

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25122] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1619 correlate with, and may be deduced from, the identity of the target genes which GAM1619 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25123] Nucleotide sequences of the GAM1619 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1619 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1619 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1619 are further described hereinbelow with reference to Table Table1.

[25124] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1619 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25125] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1620 (GAM1620) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25126] GAM1620 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1620 was detected is described hereinabove with reference to Figs. 2-8.

[25127] GAM1620 gene, herein designated GAM GENE, and GAM1620 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25128] GAM1620 gene, herein designated GAM GENE, encodes a GAM1620 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1620 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1620 precursor RNA is designated SEQ ID:1593, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1593 is located at position 4851368 relative to contig NT_022517.13, on chromosome 3.

[25129] GAM1620 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1620 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25130] An enzyme complex designated DICER COMPLEX, dices the GAM1620 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1620 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1620 RNA is designated SEQ ID:3269, and is provided hereinbelow with reference to the sequence listing part.

[25131] GAM1620 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1620 target RNA, herein designated GAM TARGET RNA. GAM1620 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25132] GAM1620 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1620 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1620 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1620 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1620 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25133] The complementary binding of GAM1620 RNA, herein designated GAM RNA, to target binding sites on GAM1620 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1620 target RNA, herein designated GAM TARGET RNA, into GAM1620 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25134] It is appreciated that GAM1620 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1620 target genes. The mRNA of each one of this plurality of GAM1620 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1620 RNA, herein designated GAM RNA, and which when bound by GAM1620 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1620 target proteins.

[25135] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1620 gene, herein designated GAM GENE, on one or more GAM1620 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25136] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1620 correlate with, and may

be deduced from, the identity of the target genes which GAM1620 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25137] Nucleotide sequences of the GAM1620 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1620 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1620 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1620 are further described hereinbelow with reference to Table Table1.

[25138] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1620 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25139] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1621 (GAM1621) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25140] GAM1621 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1621 was detected is described hereinabove with reference to Figs. 2-8.

[25141] GAM1621 gene, herein designated GAM GENE, and GAM1621 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25142] GAM1621 gene, herein designated GAM GENE, encodes a GAM1621 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1621 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1621 precursor RNA is designated SEQ ID:1594, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1594 is located at position 11570630 relative to contig NT_008470.13, on chromosome 9.

[25143] GAM1621 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1621 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25144] An enzyme complex designated DICER COMPLEX, dices the GAM1621 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1621 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1621 RNA is designated SEQ ID:3270, and is provided hereinbelow with reference to the sequence listing part.

[25145] GAM1621 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1621 target RNA, herein designated GAM TARGET RNA. GAM1621 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, design-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[25146] GAM1621 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1621 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1621 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1621 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1621 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25147] The complementary binding of GAM1621 RNA, herein

designated GAM RNA, to target binding sites on GAM1621 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1621 target RNA, herein designated GAM TARGET RNA, into GAM1621 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25148] It is appreciated that GAM1621 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1621 target genes. The mRNA of each one of this plurality of GAM1621 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1621 RNA, herein designated GAM RNA, and which when bound by GAM1621 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1621 target proteins.

[25149] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1621 gene, herein designated GAM GENE, on one or more GAM1621 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25150] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1621 correlate with, and may be deduced from, the identity of the target genes which GAM1621 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25151] Nucleotide sequences of the GAM1621 precursor RNA, herein designated GAM PRECURSOR RNA, and of the dived GAM1621 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1621 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1621 are further described hereinbelow with reference to Table Table1.

[25152] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1621 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[25153] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1622 (GAM1622) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25154] GAM1622 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1622 was detected is described hereinabove with reference to Figs. 2-8.

[25155] GAM1622 gene, herein designated GAM GENE, and GAM1622 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25156] GAM1622 gene, herein designated GAM GENE, encodes a GAM1622 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1622 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1622 precursor RNA is designated SEQ ID:1595, and is provided hereinbelow with reference to the sequence listing part.

[25157] GAM1622 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1622 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25158] An enzyme complex designated DICER COMPLEX, dices the GAM1622 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1622 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1622 RNA is designated SEQ ID:3271, and is provided hereinbelow with reference to the sequence listing part.

[25159] GAM1622 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1622 target RNA, herein designated GAM TARGET RNA. GAM1622 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25160] GAM1622 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1622 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1622 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1622 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1622 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25161] The complementary binding of GAM1622 RNA, herein designated GAM RNA, to target binding sites on GAM1622 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1622 target RNA, herein designated GAM TARGET RNA, into GAM1622 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25162] It is appreciated that GAM1622 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1622 target genes. The mRNA of each one of this plurality of GAM1622 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1622 RNA,

herein designated GAM RNA, and which when bound by GAM1622 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1622 target proteins.

[25163] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1622 gene, herein designated GAM GENE, on one or more GAM1622 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25164] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1622 correlate with, and may be deduced from, the identity of the target genes which

GAM1622 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25165] Nucleotide sequences of the GAM1622 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1622 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1622 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1622 are further described hereinbelow with reference to Table Table1.

[25166] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1622 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25167] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1623 (GAM1623) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25168] GAM1623 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1623 was detected is described hereinabove with reference to Figs. 2–8.

[25169] GAM1623 gene, herein designated GAM GENE, and GAM1623 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25170] GAM1623 gene, herein designated GAM GENE, encodes a GAM1623 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1623 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1623 precursor RNA is designated SEQ ID:1596, and is provided hereinbelow with reference to the sequence listing part.

[25171] GAM1623 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1623 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[25172] An enzyme complex designated DICER COMPLEX, dices the GAM1623 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1623 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1623 RNA is designated SEQ ID:3272, and is provided hereinbelow with reference to the sequence listing part.

[25173] GAM1623 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1623 target RNA, herein designated GAM TARGET RNA. GAM1623 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25174] GAM1623 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1623 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1623 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1623 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1623 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25175] The complementary binding of GAM1623 RNA, herein designated GAM RNA, to target binding sites on GAM1623 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1623 target RNA, herein designated GAM TARGET RNA, into GAM1623 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25176] It is appreciated that GAM1623 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1623 target genes. The mRNA of each one of this plurality of GAM1623 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1623 RNA, herein designated GAM RNA, and which when bound by GAM1623 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1623 target proteins.

[25177] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1623 gene, herein designated GAM GENE, on one or more GAM1623 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25178] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1623 correlate with, and may be deduced from, the identity of the target genes which GAM1623 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25179] Nucleotide sequences of the GAM1623 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1623 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1623 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1623 are further described hereinbelow with reference to Table Table1.

[25180] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1623 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25181] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1624 (GAM1624) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25182] GAM1624 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1624 was detected is described hereinabove with reference to Figs. 2-8.

[25183] GAM1624 gene, herein designated GAM GENE, and GAM1624 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25184] GAM1624 gene, herein designated GAM GENE, encodes a GAM1624 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1624 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1624 precursor RNA is designated SEQ ID:1597, and is provided hereinbelow with

reference to the sequence listing part. Nucleotide sequence SEQ ID:1597 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[25185] GAM1624 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1624 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25186] An enzyme complex designated DICER COMPLEX, dices the GAM1624 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1624 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1624 RNA is designated SEQ ID:3273, and

is provided hereinbelow with reference to the sequence listing part.

[25187] GAM1624 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1624 target RNA, herein designated GAM TARGET RNA. GAM1624 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25188] GAM1624 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1624 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1624 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1624 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1624 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25189] The complementary binding of GAM1624 RNA, herein designated GAM RNA, to target binding sites on GAM1624 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1624 target RNA, herein designated GAM TARGET RNA, into GAM1624 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25190] It is appreciated that GAM1624 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1624 target genes. The mRNA of each one of this plurality of GAM1624 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1624 RNA, herein designated GAM RNA, and which when bound by

GAM1624 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1624 target proteins.

[25191] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1624 gene, herein designated GAM GENE, on one or more GAM1624 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25192] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1624 correlate with, and may be deduced from, the identity of the target genes which GAM1624 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[25193] Nucleotide sequences of the GAM1624 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1624 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1624 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1624 are further described hereinbelow with reference to Table Table1.

[25194] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1624 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25195] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1625 (GAM1625) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25196] GAM1625 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1625 was detected is described hereinabove

with reference to Figs. 2–8.

[25197] GAM1625 gene, herein designated GAM GENE, and GAM1625 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25198] GAM1625 gene, herein designated GAM GENE, encodes a GAM1625 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1625 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1625 precursor RNA is designated SEQ ID:1598, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1598 is located at position 56616163 relative to contig NT_026437.9, on chromosome 14.

[25199] GAM1625 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1625 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25200] An enzyme complex designated DICER COMPLEX, dices the GAM1625 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1625 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1625 RNA is designated SEQ ID:3274, and is provided hereinbelow with reference to the sequence listing part.

[25201] GAM1625 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1625 target RNA, herein designated GAM TARGET RNA. GAM1625 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25202] GAM1625 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1625 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1625 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1625 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1625 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25203] The complementary binding of GAM1625 RNA, herein designated GAM RNA, to target binding sites on GAM1625 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1625 target RNA, herein designated GAM TARGET RNA, into GAM1625 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25204] It is appreciated that GAM1625 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1625 target genes. The mRNA of each one of this plurality of GAM1625 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1625 RNA, herein designated GAM RNA, and which when bound by GAM1625 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1625 target proteins.

[25205] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1625 gene, herein designated GAM GENE, on one or more GAM1625 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25206] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1625 correlate with, and may be deduced from, the identity of the target genes which GAM1625 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25207] Nucleotide sequences of the GAM1625 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1625 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1625 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1625 are further described hereinbelow with reference to Table Table1.

[25208] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1625 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[25209] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1626 (GAM1626) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25210] GAM1626 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1626 was detected is described hereinabove with reference to Figs. 2-8.

[25211] GAM1626 gene, herein designated GAM GENE, and GAM1626 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25212] GAM1626 gene, herein designated GAM GENE, encodes a GAM1626 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1626 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1626 precursor RNA is

designated SEQ ID:1599, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1599 is located at position 4540528 relative to contig NT_009775.11, on chromosome 12.

[25213] GAM1626 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1626 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25214] An enzyme complex designated DICER COMPLEX, dices the GAM1626 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1626 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1626 RNA is designated SEQ ID:3275, and is provided hereinbelow with reference to the sequence listing part.

[25215] GAM1626 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1626 target RNA, herein designated GAM TARGET RNA. GAM1626 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25216] GAM1626 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1626 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1626 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1626 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1626 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25217] The complementary binding of GAM1626 RNA, herein designated GAM RNA, to target binding sites on GAM1626 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1626 target RNA, herein designated GAM TARGET RNA, into GAM1626 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25218] It is appreciated that GAM1626 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1626 target genes. The mRNA of each one of this plurality of GAM1626 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1626 RNA,

herein designated GAM RNA, and which when bound by GAM1626 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1626 target proteins.

[25219] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1626 gene, herein designated GAM GENE, on one or more GAM1626 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25220] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1626 correlate with, and may be deduced from, the identity of the target genes which

GAM1626 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25221] Nucleotide sequences of the GAM1626 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1626 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1626 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1626 are further described hereinbelow with reference to Table Table1.

[25222] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1626 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25223] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1627 (GAM1627) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25224] GAM1627 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1627 was detected is described hereinabove with reference to Figs. 2–8.

[25225] GAM1627 gene, herein designated GAM GENE, and GAM1627 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25226] GAM1627 gene, herein designated GAM GENE, encodes a GAM1627 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1627 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1627 precursor RNA is designated SEQ ID:1600, and is provided hereinbelow with reference to the sequence listing part.

[25227] GAM1627 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1627 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[25228] An enzyme complex designated DICER COMPLEX, dices the GAM1627 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1627 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1627 RNA is designated SEQ ID:3276, and is provided hereinbelow with reference to the sequence listing part.

[25229] GAM1627 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1627 target RNA, herein designated GAM TARGET RNA. GAM1627 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25230] GAM1627 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1627 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1627 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1627 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1627 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25231] The complementary binding of GAM1627 RNA, herein designated GAM RNA, to target binding sites on GAM1627 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1627 target RNA, herein designated GAM TARGET RNA, into GAM1627 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25232] It is appreciated that GAM1627 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1627 target genes. The mRNA of each one of this plurality of GAM1627 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1627 RNA, herein designated GAM RNA, and which when bound by GAM1627 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1627 target proteins.

[25233] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1627 gene, herein designated GAM GENE, on one or more GAM1627 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25234] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1627 correlate with, and may be deduced from, the identity of the target genes which GAM1627 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25235] Nucleotide sequences of the GAM1627 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1627 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1627 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1627 are further described hereinbelow with reference to Table Table1.

[25236] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1627 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25237] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1628 (GAM1628) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25238] GAM1628 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1628 was detected is described hereinabove with reference to Figs. 2-8.

[25239] GAM1628 gene, herein designated GAM GENE, and GAM1628 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25240] GAM1628 gene, herein designated GAM GENE, encodes a GAM1628 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1628 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1628 precursor RNA is designated SEQ ID:1601, and is provided hereinbelow with

reference to the sequence listing part. Nucleotide sequence SEQ ID:1601 is located at position 280476 relative to contig NT_007758.8, on chromosome 7.

[25241] GAM1628 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1628 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25242] An enzyme complex designated DICER COMPLEX, dices the GAM1628 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1628 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1628 RNA is designated SEQ ID:3277, and

is provided hereinbelow with reference to the sequence listing part.

[25243] GAM1628 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1628 target RNA, herein designated GAM TARGET RNA. GAM1628 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25244] GAM1628 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1628 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1628 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1628 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1628 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25245] The complementary binding of GAM1628 RNA, herein designated GAM RNA, to target binding sites on GAM1628 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1628 target RNA, herein designated GAM TARGET RNA, into GAM1628 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25246] It is appreciated that GAM1628 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1628 target genes. The mRNA of each one of this plurality of GAM1628 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1628 RNA, herein designated GAM RNA, and which when bound by

GAM1628 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1628 target proteins.

[25247] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1628 gene, herein designated GAM GENE, on one or more GAM1628 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25248] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1628 correlate with, and may be deduced from, the identity of the target genes which GAM1628 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[25249] Nucleotide sequences of the GAM1628 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1628 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1628 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1628 are further described hereinbelow with reference to Table Table1.

[25250] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1628 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25251] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1629 (GAM1629) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25252] GAM1629 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1629 was detected is described hereinabove

with reference to Figs. 2-8.

[25253] GAM1629 gene, herein designated GAM GENE, and GAM1629 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25254] GAM1629 gene, herein designated GAM GENE, encodes a GAM1629 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1629 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1629 precursor RNA is designated SEQ ID:1602, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1602 is located at position 15567257 relative to contig NT_007592.11, on chromosome 6.

[25255] GAM1629 has 20 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[25256] SEQ ID:99575 detected in mouse EST Accession BG092976.1.

[25257] SEQ ID:99576 detected in mouse EST Accession

AA798467.1.

[25258] SEQ ID:99577 detected in mouse EST Accession
BG147005.1.

[25259] SEQ ID:99578 detected in mouse EST Accession
BE311050.1.

[25260] SEQ ID:99579 detected in mouse EST Accession
BE625094.1.

[25261] SEQ ID:99580 detected in mouse EST Accession
BG914583.1.

[25262] SEQ ID:99581 detected in mouse EST Accession
BF784199.1.

[25263] SEQ ID:99582 detected in mouse EST Accession
BG975946.1.

[25264] SEQ ID:99583 detected in mouse EST Accession
BI689042.1.

[25265] SEQ ID:99584 detected in mouse EST Accession
BI696541.1.

[25266] SEQ ID:99585 detected in mouse EST Accession
BF140373.1.

[25267] SEQ ID:99589 detected in mouse EST Accession
AI194277.1.

[25268] SEQ ID:99590 detected in mouse EST Accession
BG803992.1.

[25269] SEQ ID:99592 detected in mouse EST Accession
BF465841.1.

[25270] SEQ ID:99593 detected in mouse EST Accession
AA798123.1.

[25271] SEQ ID:99594 detected in mouse EST Accession
BG148023.1.

[25272] SEQ ID:99595 detected in mouse EST Accession
AI316639.1.

[25273] SEQ ID:99596 detected in mouse EST Accession
BI659175.1.

[25274] SEQ ID:99597 detected in mouse EST Accession
BB067326.2.

[25275] SEQ ID:99598 detected in mouse EST Accession
BI080618.1.

[25276] GAM1629 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1629 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[25277] An enzyme complex designated DICER COMPLEX, dices the GAM1629 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1629 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1629 RNA is designated SEQ ID:3278, and is provided hereinbelow with reference to the sequence listing part.

[25278] GAM1629 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1629 target RNA, herein designated GAM TARGET RNA. GAM1629 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25279] GAM1629 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1629 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1629 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1629 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1629 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25280] The complementary binding of GAM1629 RNA, herein designated GAM RNA, to target binding sites on GAM1629 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1629 target RNA, herein designated GAM TARGET RNA, into GAM1629 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25281] It is appreciated that GAM1629 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1629 target genes. The mRNA of each one of this plurality of GAM1629 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1629 RNA, herein designated GAM RNA, and which when bound by GAM1629 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1629 target proteins.

[25282] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1629 gene, herein designated GAM GENE, on one or more GAM1629 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25283] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1629 correlate with, and may be deduced from, the identity of the target genes which GAM1629 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25284] Nucleotide sequences of the GAM1629 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1629 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1629 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1629 are further described hereinbelow with reference to Table Table1.

[25285] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1629 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25286] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1630 (GAM1630) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25287] GAM1630 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1630 was detected is described hereinabove with reference to Figs. 2-8.

[25288] GAM1630 gene, herein designated GAM GENE, and GAM1630 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25289] GAM1630 gene, herein designated GAM GENE, encodes a GAM1630 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1630 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1630 precursor RNA is designated SEQ ID:1603, and is provided hereinbelow with

reference to the sequence listing part. Nucleotide sequence SEQ ID:1603 is located at position 9039266 relative to contig NT_030059.8, on chromosome 10.

[25290] GAM1630 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1630 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25291] An enzyme complex designated DICER COMPLEX, dices the GAM1630 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1630 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1630 RNA is designated SEQ ID:3279, and

is provided hereinbelow with reference to the sequence listing part.

[25292] GAM1630 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1630 target RNA, herein designated GAM TARGET RNA. GAM1630 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25293] GAM1630 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1630 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1630 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1630 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1630 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25294] The complementary binding of GAM1630 RNA, herein designated GAM RNA, to target binding sites on GAM1630 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1630 target RNA, herein designated GAM TARGET RNA, into GAM1630 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25295] It is appreciated that GAM1630 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1630 target genes. The mRNA of each one of this plurality of GAM1630 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1630 RNA, herein designated GAM RNA, and which when bound by

GAM1630 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1630 target proteins.

[25296] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1630 gene, herein designated GAM GENE, on one or more GAM1630 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25297] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1630 correlate with, and may be deduced from, the identity of the target genes which GAM1630 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[25298] Nucleotide sequences of the GAM1630 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1630 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1630 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1630 are further described hereinbelow with reference to Table Table1.

[25299] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1630 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25300] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1631 (GAM1631) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25301] GAM1631 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1631 was detected is described hereinabove

with reference to Figs. 2–8.

[25302] GAM1631 gene, herein designated GAM GENE, and GAM1631 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25303] GAM1631 gene, herein designated GAM GENE, encodes a GAM1631 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1631 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1631 precursor RNA is designated SEQ ID:1604, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1604 is located at position 2907543 relative to contig NT_015805.11, on chromosome 2.

[25304] GAM1631 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1631 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25305] An enzyme complex designated DICER COMPLEX, dices the GAM1631 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1631 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1631 RNA is designated SEQ ID:3280, and is provided hereinbelow with reference to the sequence listing part.

[25306] GAM1631 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1631 target RNA, herein designated GAM TARGET RNA. GAM1631 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25307] GAM1631 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1631 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1631 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1631 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1631 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25308] The complementary binding of GAM1631 RNA, herein designated GAM RNA, to target binding sites on GAM1631 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1631 target RNA, herein designated GAM TARGET RNA, into GAM1631 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25309] It is appreciated that GAM1631 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1631 target genes. The mRNA of each one of this plurality of GAM1631 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1631 RNA, herein designated GAM RNA, and which when bound by GAM1631 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1631 target proteins.

[25310] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1631 gene, herein designated GAM GENE, on one or more GAM1631 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25311] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1631 correlate with, and may be deduced from, the identity of the target genes which GAM1631 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25312] Nucleotide sequences of the GAM1631 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1631 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1631 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1631 are further described hereinbelow with reference to Table Table1.

[25313] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1631 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[25314] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1632 (GAM1632) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25315] GAM1632 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1632 was detected is described hereinabove with reference to Figs. 2-8.

[25316] GAM1632 gene, herein designated GAM GENE, and GAM1632 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25317] GAM1632 gene, herein designated GAM GENE, encodes a GAM1632 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1632 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1632 precursor RNA is

designated SEQ ID:1605, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1605 is located at position 2383351 relative to contig NT_035212.2, on chromosome 12.

[25318] GAM1632 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1632 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25319] An enzyme complex designated DICER COMPLEX, dices the GAM1632 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1632 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1632 RNA is designated SEQ ID:3281, and is provided hereinbelow with reference to the sequence listing part.

[25320] GAM1632 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1632 target RNA, herein designated GAM TARGET RNA. GAM1632 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25321] GAM1632 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1632 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1632 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1632 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1632 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25322] The complementary binding of GAM1632 RNA, herein designated GAM RNA, to target binding sites on GAM1632 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1632 target RNA, herein designated GAM TARGET RNA, into GAM1632 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25323] It is appreciated that GAM1632 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1632 target genes. The mRNA of each one of this plurality of GAM1632 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1632 RNA,

herein designated GAM RNA, and which when bound by GAM1632 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1632 target proteins.

[25324] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1632 gene, herein designated GAM GENE, on one or more GAM1632 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25325] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1632 correlate with, and may be deduced from, the identity of the target genes which

GAM1632 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25326] Nucleotide sequences of the GAM1632 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1632 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1632 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1632 are further described hereinbelow with reference to Table Table1.

[25327] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1632 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25328] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1633 (GAM1633) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25329] GAM1633 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1633 was detected is described hereinabove with reference to Figs. 2–8.

[25330] GAM1633 gene, herein designated GAM GENE, and GAM1633 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25331] GAM1633 gene, herein designated GAM GENE, encodes a GAM1633 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1633 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1633 precursor RNA is designated SEQ ID:1606, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1606 is located at position 3436496 relative to contig NT_023148.9, on chromosome 5.

[25332] GAM1633 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1633 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25333] An enzyme complex designated DICER COMPLEX, dices the GAM1633 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1633 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1633 RNA is designated SEQ ID:3282, and is provided hereinbelow with reference to the sequence listing part.

[25334] GAM1633 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1633 target RNA, herein designated GAM TARGET RNA. GAM1633 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25335] GAM1633 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1633 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1633 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1633 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1633 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25336] The complementary binding of GAM1633 RNA, herein designated GAM RNA, to target binding sites on GAM1633

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1633 target RNA, herein designated GAM TARGET RNA, into GAM1633 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25337] It is appreciated that GAM1633 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1633 target genes. The mRNA of each one of this plurality of GAM1633 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1633 RNA, herein designated GAM RNA, and which when bound by GAM1633 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1633 target proteins.

[25338] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1633 gene, herein designated GAM GENE, on one or more GAM1633 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25339] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1633 correlate with, and may be deduced from, the identity of the target genes which GAM1633 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25340] Nucleotide sequences of the GAM1633 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1633 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1633 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1633 are further described hereinbelow with reference to Table Table1.

[25341] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1633 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25342] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1634 (GAM1634) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25343] GAM1634 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1634 was detected is described hereinabove with reference to Figs. 2-8.

[25344] GAM1634 gene, herein designated GAM GENE, and GAM1634 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25345] GAM1634 gene, herein designated GAM GENE, encodes a GAM1634 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1634 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1634 precursor RNA is designated SEQ ID:1607, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1607 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[25346] GAM1634 precursor RNA, herein designated GAM PRE-CURSORS RNA, folds onto itself, forming GAM1634 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25347] An enzyme complex designated DICER COMPLEX, dices the GAM1634 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1634 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1634 RNA is designated SEQ ID:3283, and is provided hereinbelow with reference to the sequence listing part.

[25348] GAM1634 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1634 target RNA, herein designated GAM TARGET RNA. GAM1634 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25349] GAM1634 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1634 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1634 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1634 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1634 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25350] The complementary binding of GAM1634 RNA, herein designated GAM RNA, to target binding sites on GAM1634 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1634 target RNA, herein designated GAM TARGET RNA, into GAM1634 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25351] It is appreciated that GAM1634 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1634 target genes. The mRNA of each one of this plurality of GAM1634 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1634 RNA, herein designated GAM RNA, and which when bound by GAM1634 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1634 target proteins.

[25352] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1634 gene, herein designated GAM GENE, on one or more GAM1634 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25353] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1634 correlate with, and may

be deduced from, the identity of the target genes which GAM1634 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25354] Nucleotide sequences of the GAM1634 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1634 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1634 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1634 are further described hereinbelow with reference to Table Table1.

[25355] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1634 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25356] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1635 (GAM1635) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25357] GAM1635 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1635 was detected is described hereinabove with reference to Figs. 2-8.

[25358] GAM1635 gene, herein designated GAM GENE, and GAM1635 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25359] GAM1635 gene, herein designated GAM GENE, encodes a GAM1635 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1635 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1635 precursor RNA is designated SEQ ID:1608, and is provided hereinbelow with reference to the sequence listing part.

[25360] GAM1635 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1635 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25361] An enzyme complex designated DICER COMPLEX, dices the GAM1635 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1635 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1635 RNA is designated SEQ ID:3284, and is provided hereinbelow with reference to the sequence listing part.

[25362] GAM1635 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1635 target RNA, herein designated GAM TARGET RNA. GAM1635 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25363] GAM1635 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1635 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1635 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1635 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1635 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25364] The complementary binding of GAM1635 RNA, herein designated GAM RNA, to target binding sites on GAM1635 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1635 target RNA, herein designated GAM TARGET RNA, into GAM1635 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25365] It is appreciated that GAM1635 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1635 target genes. The mRNA of each one of this plurality of GAM1635 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1635 RNA, herein designated GAM RNA, and which when bound by GAM1635 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1635 target proteins.

[25366] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1635 gene, herein designated GAM GENE, on one or more GAM1635 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25367] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1635 correlate with, and may be deduced from, the identity of the target genes which GAM1635 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25368] Nucleotide sequences of the GAM1635 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1635 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1635 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1635 are further described hereinbelow with reference to Table Table1.

[25369] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1635 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[25370] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1636 (GAM1636) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25371] GAM1636 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1636 was detected is described hereinabove with reference to Figs. 2-8.

[25372] GAM1636 gene, herein designated GAM GENE, and GAM1636 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25373] GAM1636 gene, herein designated GAM GENE, encodes a GAM1636 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1636 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1636 precursor RNA is

designated SEQ ID:1609, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1609 is located at position 808824 relative to contig NT_025004.11, on chromosome 18.

[25374] GAM1636 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1636 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25375] An enzyme complex designated DICER COMPLEX, dices the GAM1636 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1636 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1636 RNA is designated SEQ ID:3285, and is provided hereinbelow with reference to the sequence listing part.

[25376] GAM1636 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1636 target RNA, herein designated GAM TARGET RNA. GAM1636 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25377] GAM1636 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1636 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1636 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1636 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1636 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25378] The complementary binding of GAM1636 RNA, herein designated GAM RNA, to target binding sites on GAM1636 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1636 target RNA, herein designated GAM TARGET RNA, into GAM1636 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25379] It is appreciated that GAM1636 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1636 target genes. The mRNA of each one of this plurality of GAM1636 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1636 RNA,

herein designated GAM RNA, and which when bound by GAM1636 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1636 target proteins.

[25380] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1636 gene, herein designated GAM GENE, on one or more GAM1636 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25381] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1636 correlate with, and may be deduced from, the identity of the target genes which

GAM1636 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25382] Nucleotide sequences of the GAM1636 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1636 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1636 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1636 are further described hereinbelow with reference to Table Table1.

[25383] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1636 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25384] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1637 (GAM1637) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25385] GAM1637 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1637 was detected is described hereinabove with reference to Figs. 2–8.

[25386] GAM1637 gene, herein designated GAM GENE, and GAM1637 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25387] GAM1637 gene, herein designated GAM GENE, encodes a GAM1637 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1637 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1637 precursor RNA is designated SEQ ID:1610, and is provided hereinbelow with reference to the sequence listing part.

[25388] GAM1637 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1637 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[25389] An enzyme complex designated DICER COMPLEX, dices the GAM1637 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1637 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1637 RNA is designated SEQ ID:3286, and is provided hereinbelow with reference to the sequence listing part.

[25390] GAM1637 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1637 target RNA, herein designated GAM TARGET RNA. GAM1637 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25391] GAM1637 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1637 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1637 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1637 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1637 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25392] The complementary binding of GAM1637 RNA, herein designated GAM RNA, to target binding sites on GAM1637 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1637 target RNA, herein designated GAM TARGET RNA, into GAM1637 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25393] It is appreciated that GAM1637 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1637 target genes. The mRNA of each one of this plurality of GAM1637 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1637 RNA, herein designated GAM RNA, and which when bound by GAM1637 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1637 target proteins.

[25394] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1637 gene, herein designated GAM GENE, on one or more GAM1637 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25395] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1637 correlate with, and may be deduced from, the identity of the target genes which GAM1637 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25396] Nucleotide sequences of the GAM1637 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1637 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1637 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1637 are further described hereinbelow with reference to Table Table1.

[25397] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1637 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25398] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1638 (GAM1638) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25399] GAM1638 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1638 was detected is described hereinabove with reference to Figs. 2-8.

[25400] GAM1638 gene, herein designated GAM GENE, and GAM1638 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25401] GAM1638 gene, herein designated GAM GENE, encodes a GAM1638 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1638 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1638 precursor RNA is designated SEQ ID:1611, and is provided hereinbelow with

reference to the sequence listing part.

[25402] GAM1638 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1638 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25403] An enzyme complex designated DICER COMPLEX, dices the GAM1638 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1638 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1638 RNA is designated SEQ ID:3287, and is provided hereinbelow with reference to the sequence listing part.

[25404] GAM1638 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1638 target RNA, herein designated GAM TARGET RNA. GAM1638 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25405] GAM1638 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1638 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1638 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1638 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a

GAM1638 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25406] The complementary binding of GAM1638 RNA, herein designated GAM RNA, to target binding sites on GAM1638 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1638 target RNA, herein designated GAM TARGET RNA, into GAM1638 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25407] It is appreciated that GAM1638 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1638 target genes. The mRNA of each one of this plurality of GAM1638 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1638 RNA, herein designated GAM RNA, and which when bound by GAM1638 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1638

target proteins.

[25408] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1638 gene, herein designated GAM GENE, on one or more GAM1638 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25409] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1638 correlate with, and may be deduced from, the identity of the target genes which GAM1638 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25410] Nucleotide sequences of the GAM1638 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM1638 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1638 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1638 are further described hereinbelow with reference to Table Table1.

[25411] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1638 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25412] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1639 (GAM1639) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25413] GAM1639 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1639 was detected is described hereinabove with reference to Figs. 2-8.

[25414] GAM1639 gene, herein designated GAM GENE, and

GAM1639 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25415] GAM1639 gene, herein designated GAM GENE, encodes a GAM1639 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1639 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1639 precursor RNA is designated SEQ ID:1612, and is provided hereinbelow with reference to the sequence listing part.

[25416] GAM1639 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1639 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25417] An enzyme complex designated DICER COMPLEX, dices the GAM1639 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1639 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1639 RNA is designated SEQ ID:3288, and is provided hereinbelow with reference to the sequence listing part.

[25418] GAM1639 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1639 target RNA, herein designated GAM TARGET RNA. GAM1639 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25419] GAM1639 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1639 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1639

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1639 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1639 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25420] The complementary binding of GAM1639 RNA, herein designated GAM RNA, to target binding sites on GAM1639 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1639 target RNA, herein designated GAM TARGET RNA, into GAM1639 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[25421] It is appreciated that GAM1639 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1639 target genes. The mRNA of each one of this plurality of GAM1639 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1639 RNA, herein designated GAM RNA, and which when bound by GAM1639 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1639 target proteins.

[25422] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1639 gene, herein designated GAM GENE, on one or more GAM1639 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25423] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1639 correlate with, and may be deduced from, the identity of the target genes which GAM1639 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25424] Nucleotide sequences of the GAM1639 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1639 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1639 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1639 are further described hereinbelow with reference to Table Table1.

[25425] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1639 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25426] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1640 (GAM1640) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25427] GAM1640 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1640 was detected is described hereinabove with reference to Figs. 2-8.

[25428] GAM1640 gene, herein designated GAM GENE, and GAM1640 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25429] GAM1640 gene, herein designated GAM GENE, encodes a GAM1640 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1640 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1640 precursor RNA is designated SEQ ID:1613, and is provided hereinbelow with reference to the sequence listing part.

[25430] GAM1640 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1640 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25431] An enzyme complex designated DICER COMPLEX, dices the GAM1640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1640 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1640 RNA is designated SEQ ID:3289, and is provided hereinbelow with reference to the sequence listing part.

[25432] GAM1640 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1640 target RNA, herein designated GAM TARGET

RNA. GAM1640 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25433] GAM1640 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1640 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1640 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1640 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1640 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25434] The complementary binding of GAM1640 RNA, herein designated GAM RNA, to target binding sites on GAM1640 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1640 target RNA, herein designated GAM TARGET RNA, into GAM1640 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25435] It is appreciated that GAM1640 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1640 target genes. The mRNA of each one of this plurality of GAM1640 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1640 RNA, herein designated GAM RNA, and which when bound by GAM1640 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1640 target proteins.

[25436] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1640 gene, herein designated GAM GENE, on one or more GAM1640 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25437] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1640 correlate with, and may be deduced from, the identity of the target genes which GAM1640 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25438] Nucleotide sequences of the GAM1640 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1640 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1640 are further described hereinbelow with reference to Table Table1.

[25439] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1640 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25440] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1641 (GAM1641) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25441] GAM1641 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1641 was detected is described hereinabove with reference to Figs. 2-8.

[25442] GAM1641 gene, herein designated GAM GENE, and GAM1641 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25443] GAM1641 gene, herein designated GAM GENE, encodes a

GAM1641 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1641 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1641 precursor RNA is designated SEQ ID:1614, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1614 is located at position 2081201 relative to contig NT_011109.13, on chromosome 19.

[25444] GAM1641 has 4 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[25445] SEQ ID:99996 detected in mouse EST Accession AA606484.1.

[25446] SEQ ID:99997 detected in mouse EST Accession AA541834.1.

[25447] SEQ ID:99998 detected in mouse EST Accession AA097502.1.

[25448] SEQ ID:99999 detected in mouse EST Accession BI111547.1.

[25449] GAM1641 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1641 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25450] An enzyme complex designated DICER COMPLEX, dices the GAM1641 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1641 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1641 RNA is designated SEQ ID:3290, and is provided hereinbelow with reference to the sequence listing part.

[25451] GAM1641 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM1641 target RNA, herein designated GAM TARGET RNA. GAM1641 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25452] GAM1641 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1641 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1641 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1641 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1641 target RNA, herein designated GAM TARGET

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25453] The complementary binding of GAM1641 RNA, herein designated GAM RNA, to target binding sites on GAM1641 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1641 target RNA, herein designated GAM TARGET RNA, into GAM1641 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25454] It is appreciated that GAM1641 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1641 target genes. The mRNA of each one of this plurality of GAM1641 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1641 RNA, herein designated GAM RNA, and which when bound by GAM1641 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1641 target proteins.

[25455] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1641 gene, herein designated GAM GENE, on one or more GAM1641 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25456] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1641 correlate with, and may be deduced from, the identity of the target genes which GAM1641 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25457] Nucleotide sequences of the GAM1641 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM1641 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1641 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1641 are further described hereinbelow with reference to Table Table1.

[25458] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1641 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25459] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1642 (GAM1642) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25460] GAM1642 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1642 was detected is described hereinabove with reference to Figs. 2-8.

[25461] GAM1642 gene, herein designated GAM GENE, and GAM1642 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[25462] GAM1642 gene, herein designated GAM GENE, encodes a GAM1642 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1642 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1642 precursor RNA is designated SEQ ID:1615, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1615 is located at position 5764678 relative to contig NT_008984.13, on chromosome 11.

[25463] GAM1642 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1642 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25464] An enzyme complex designated DICER COMPLEX, dices

the GAM1642 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1642 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1642 RNA is designated SEQ ID:3291, and is provided hereinbelow with reference to the sequence listing part.

[25465] GAM1642 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1642 target RNA, herein designated GAM TARGET RNA. GAM1642 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25466] GAM1642 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1642 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1642 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1642 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1642 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25467] The complementary binding of GAM1642 RNA, herein designated GAM RNA, to target binding sites on GAM1642 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1642 target RNA, herein designated GAM TARGET RNA, into GAM1642 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25468] It is appreciated that GAM1642 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1642 target genes. The mRNA of each one of this plurality of GAM1642 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1642 RNA, herein designated GAM RNA, and which when bound by GAM1642 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1642 target proteins.

[25469] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1642 gene, herein designated GAM GENE, on one or more GAM1642 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25470] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1642 correlate with, and may be deduced from, the identity of the target genes which GAM1642 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25471] Nucleotide sequences of the GAM1642 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1642 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1642 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1642 are further described hereinbelow with reference to Table Table1.

[25472] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1642 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25473] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1643 (GAM1643) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25474] GAM1643 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1643 was detected is described hereinabove with reference to Figs. 2-8.

[25475] GAM1643 gene, herein designated GAM GENE, and GAM1643 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25476] GAM1643 gene, herein designated GAM GENE, encodes a GAM1643 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1643 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1643 precursor RNA is designated SEQ ID:1616, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1616 is located at position 3434852 rela-

tive to contig NT_009714.13, on chromosome 12.

[25477] GAM1643 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:99524, which mouse homolog is detected in mouse EST accession BG288438.1.

[25478] GAM1643 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1643 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25479] An enzyme complex designated DICER COMPLEX, dices the GAM1643 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1643 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1643 RNA is designated SEQ ID:3292, and is provided hereinbelow with reference to the sequence listing part.

[25480] GAM1643 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1643 target RNA, herein designated GAM TARGET RNA. GAM1643 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25481] GAM1643 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1643 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1643 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1643 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1643 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25482] The complementary binding of GAM1643 RNA, herein designated GAM RNA, to target binding sites on GAM1643 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1643 target RNA, herein designated GAM TARGET RNA, into GAM1643 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25483] It is appreciated that GAM1643 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1643 target genes. The mRNA of each one of this plurality of GAM1643 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1643 RNA, herein designated GAM RNA, and which when bound by GAM1643 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1643 target proteins.

[25484] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1643 gene, herein designated GAM GENE, on one or more GAM1643 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25485] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1643 correlate with, and may be deduced from, the identity of the target genes which GAM1643 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25486] Nucleotide sequences of the GAM1643 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1643 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1643 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1643 are further described hereinbelow with reference to Table Table1.

[25487] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1643 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25488] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1644 (GAM1644) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25489] GAM1644 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1644 was detected is described hereinabove with reference to Figs. 2-8.

[25490] GAM1644 gene, herein designated GAM GENE, and GAM1644 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25491] GAM1644 gene, herein designated GAM GENE, encodes a GAM1644 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1644 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1644 precursor RNA is designated SEQ ID:1617, and is provided hereinbelow with reference to the sequence listing part.

[25492] GAM1644 has 20 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[25493] SEQ ID:98160 detected in mouse EST Accession AA623023.1.

[25494] SEQ ID:98161 detected in mouse EST Accession
AA561578.1.

[25495] SEQ ID:98162 detected in mouse EST Accession
BF453421.1.

[25496] SEQ ID:98163 detected in mouse EST Accession
BE687835.1.

[25497] SEQ ID:98164 detected in mouse EST Accession
AA177678.1.

[25498] SEQ ID:98165 detected in mouse EST Accession
BE448444.1.

[25499] SEQ ID:98166 detected in mouse EST Accession
AA499506.1.

[25500] SEQ ID:98167 detected in mouse EST Accession
AI551780.1.

[25501] SEQ ID:98168 detected in mouse EST Accession
BG228324.1.

- [25502] SEQ ID:98169 detected in mouse EST Accession
BB620404.1.
- [25503] SEQ ID:98170 detected in mouse EST Accession
AA111127.1.
- [25504] SEQ ID:98171 detected in mouse EST Accession
AA929520.1.
- [25505] SEQ ID:98172 detected in mouse EST Accession
BE634222.1.
- [25506] SEQ ID:98173 detected in mouse EST Accession
BE692018.1.
- [25507] SEQ ID:98174 detected in mouse EST Accession
BI647812.1.
- [25508] SEQ ID:98175 detected in mouse EST Accession
BF722531.1.
- [25509] SEQ ID:98176 detected in mouse EST Accession
BG071829.1.
- [25510] SEQ ID:98177 detected in mouse EST Accession
AI118571.1.
- [25511] SEQ ID:98178 detected in mouse EST Accession
BI689430.1.
- [25512] SEQ ID:98179 detected in mouse EST Accession
BI248537.1.
- [25513] GAM1644 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1644 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25514] An enzyme complex designated DICER COMPLEX, dices the GAM1644 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1644 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1644 RNA is designated SEQ ID:3293, and is provided hereinbelow with reference to the sequence listing part.

[25515] GAM1644 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1644 target RNA, herein designated GAM TARGET RNA. GAM1644 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25516] GAM1644 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1644 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1644 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1644 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1644 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25517] The complementary binding of GAM1644 RNA, herein designated GAM RNA, to target binding sites on GAM1644 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1644 target RNA, herein designated GAM TARGET RNA, into GAM1644 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25518] It is appreciated that GAM1644 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1644 target genes. The mRNA of each one of this plurality of GAM1644 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1644 RNA, herein designated GAM RNA, and which when bound by GAM1644 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1644 target proteins.

[25519] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1644 gene, herein designated GAM GENE, on one or more GAM1644 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25520] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1644 correlate with, and may be deduced from, the identity of the target genes which GAM1644 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25521] Nucleotide sequences of the GAM1644 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1644 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1644 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1644 are further described hereinbelow with reference to Table Table1.

[25522] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1644 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25523] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1645 (GAM1645) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25524] GAM1645 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1645 was detected is described hereinabove with reference to Figs. 2-8.

[25525] GAM1645 gene, herein designated GAM GENE, and GAM1645 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25526] GAM1645 gene, herein designated GAM GENE, encodes a GAM1645 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1645 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1645 precursor RNA is designated SEQ ID:1618, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1618 is located at position 1698742 relative to contig NT_028309.8, on chromosome 11.

[25527] GAM1645 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1645 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25528] An enzyme complex designated DICER COMPLEX, dices the GAM1645 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1645 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1645 RNA is designated SEQ ID:3294, and is provided hereinbelow with reference to the sequence listing part.

[25529] GAM1645 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1645 target RNA, herein designated GAM TARGET RNA. GAM1645 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25530] GAM1645 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1645 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1645

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1645 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1645 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25531] The complementary binding of GAM1645 RNA, herein designated GAM RNA, to target binding sites on GAM1645 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1645 target RNA, herein designated GAM TARGET RNA, into GAM1645 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[25532] It is appreciated that GAM1645 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1645 target genes. The mRNA of each one of this plurality of GAM1645 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1645 RNA, herein designated GAM RNA, and which when bound by GAM1645 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1645 target proteins.

[25533] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1645 gene, herein designated GAM GENE, on one or more GAM1645 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25534] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1645 correlate with, and may be deduced from, the identity of the target genes which GAM1645 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25535] Nucleotide sequences of the GAM1645 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1645 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1645 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1645 are further described hereinbelow with reference to Table Table1.

[25536] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1645 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25537] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1646 (GAM1646) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25538] GAM1646 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1646 was detected is described hereinabove with reference to Figs. 2-8.

[25539] GAM1646 gene, herein designated GAM GENE, and GAM1646 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25540] GAM1646 gene, herein designated GAM GENE, encodes a GAM1646 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1646 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1646 precursor RNA is designated SEQ ID:1619, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1619 is located at position 6294511 relative to contig NT_024981.11, on chromosome 18.

[25541] GAM1646 has 15 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[25542] SEQ ID:99993 detected in mouse EST Accession BF719273.1.

[25543] SEQ ID:99994 detected in mouse EST Accession BF020008.1.

[25544] SEQ ID:99995 detected in mouse EST Accession BB615397.1.

[25545] SEQ ID:98180 detected in mouse EST Accession AW743974.1.

[25546] SEQ ID:98181 detected in mouse EST Accession BE947979.1.

[25547] SEQ ID:98182 detected in mouse EST Accession BF463146.1.

[25548] SEQ ID:98183 detected in mouse EST Accession BF718970.1.

[25549] SEQ ID:98184 detected in mouse EST Accession AW456243.1.

[25550] SEQ ID:98185 detected in mouse EST Accession AW494497.1.

[25551] SEQ ID:98186 detected in mouse EST Accession
AW987984.1.

[25552] SEQ ID:98187 detected in mouse EST Accession
BB624634.1.

[25553] SEQ ID:98188 detected in mouse EST Accession
AW987905.1.

[25554] SEQ ID:98189 detected in mouse EST Accession
BI111596.1.

[25555] SEQ ID:98190 detected in mouse EST Accession
BE915985.1.

[25556] SEQ ID:98191 detected in mouse EST Accession
BF472656.1.

[25557] GAM1646 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1646 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25558] An enzyme complex designated DICER COMPLEX, dices

the GAM1646 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1646 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1646 RNA is designated SEQ ID:3295, and is provided hereinbelow with reference to the sequence listing part.

[25559] GAM1646 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1646 target RNA, herein designated GAM TARGET RNA. GAM1646 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25560] GAM1646 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1646 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1646 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1646 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1646 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25561] The complementary binding of GAM1646 RNA, herein designated GAM RNA, to target binding sites on GAM1646 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1646 target RNA, herein designated GAM TARGET RNA, into GAM1646 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25562] It is appreciated that GAM1646 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1646 target genes. The mRNA of each one of this plurality of GAM1646 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1646 RNA, herein designated GAM RNA, and which when bound by GAM1646 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1646 target proteins.

[25563] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1646 gene, herein designated GAM GENE, on one or more GAM1646 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25564] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1646 correlate with, and may be deduced from, the identity of the target genes which GAM1646 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25565] Nucleotide sequences of the GAM1646 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1646 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1646 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1646 are further described hereinbelow with reference to Table Table1.

[25566] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1646 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25567] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1647 (GAM1647) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25568] GAM1647 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1647 was detected is described hereinabove with reference to Figs. 2-8.

[25569] GAM1647 gene, herein designated GAM GENE, and GAM1647 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25570] GAM1647 gene, herein designated GAM GENE, encodes a GAM1647 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1647 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1647 precursor RNA is designated SEQ ID:1620, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1620 is located at position 2349674 rela-

tive to contig NT_021907.13, on chromosome 1.

[25571] GAM1647 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1647 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25572] An enzyme complex designated DICER COMPLEX, dices the GAM1647 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1647 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1647 RNA is designated SEQ ID:3296, and is provided hereinbelow with reference to the sequence listing part.

[25573] GAM1647 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1647 target RNA, herein designated GAM TARGET RNA. GAM1647 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25574] GAM1647 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1647 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1647 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1647 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a

GAM1647 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25575] The complementary binding of GAM1647 RNA, herein designated GAM RNA, to target binding sites on GAM1647 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1647 target RNA, herein designated GAM TARGET RNA, into GAM1647 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25576] It is appreciated that GAM1647 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1647 target genes. The mRNA of each one of this plurality of GAM1647 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1647 RNA, herein designated GAM RNA, and which when bound by GAM1647 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1647

target proteins.

[25577] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1647 gene, herein designated GAM GENE, on one or more GAM1647 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25578] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1647 correlate with, and may be deduced from, the identity of the target genes which GAM1647 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25579] Nucleotide sequences of the GAM1647 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM1647 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1647 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1647 are further described hereinbelow with reference to Table Table1.

[25580] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1647 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25581] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1648 (GAM1648) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25582] GAM1648 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1648 was detected is described hereinabove with reference to Figs. 2-8.

[25583] GAM1648 gene, herein designated GAM GENE, and

GAM1648 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25584] GAM1648 gene, herein designated GAM GENE, encodes a GAM1648 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1648 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1648 precursor RNA is designated SEQ ID:1621, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1621 is located at position 755864 relative to contig NT_005416.8, on chromosome 2.

[25585] GAM1648 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1648 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25586] An enzyme complex designated DICER COMPLEX, dices the GAM1648 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1648 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1648 RNA is designated SEQ ID:3297, and is provided hereinbelow with reference to the sequence listing part.

[25587] GAM1648 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1648 target RNA, herein designated GAM TARGET RNA. GAM1648 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25588] GAM1648 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1648 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1648 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1648 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1648 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25589] The complementary binding of GAM1648 RNA, herein designated GAM RNA, to target binding sites on GAM1648 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1648 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1648 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25590] It is appreciated that GAM1648 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1648 target genes. The mRNA of each one of this plurality of GAM1648 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1648 RNA, herein designated GAM RNA, and which when bound by GAM1648 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1648 target proteins.

[25591] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1648 gene, herein designated GAM GENE, on one or more GAM1648 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25592] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1648 correlate with, and may be deduced from, the identity of the target genes which GAM1648 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25593] Nucleotide sequences of the GAM1648 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1648 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1648 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1648 are further described hereinbelow with reference to Table Table1.

[25594] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1648 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[25595] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1649 (GAM1649) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25596] GAM1649 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1649 was detected is described hereinabove with reference to Figs. 2-8.

[25597] GAM1649 gene, herein designated GAM GENE, and GAM1649 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25598] GAM1649 gene, herein designated GAM GENE, encodes a GAM1649 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1649 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1649 precursor RNA is designated SEQ ID:1622, and is provided hereinbelow with reference to the sequence listing part.

[25599] GAM1649 has 13 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[25600] SEQ ID:98145 detected in mouse EST Accession BI409473.1.

[25601] SEQ ID:98146 detected in mouse EST Accession W36780.1.

[25602] SEQ ID:98147 detected in mouse EST Accession BE652434.1.

[25603] SEQ ID:98148 detected in mouse EST Accession BG861731.1.

[25604] SEQ ID:98149 detected in mouse EST Accession BE311296.1.

[25605] SEQ ID:98151 detected in mouse EST Accession AA245034.1.

[25606] SEQ ID:98152 detected in mouse EST Accession W42007.1.

[25607] SEQ ID:98153 detected in mouse EST Accession BE952277.1.

[25608] SEQ ID:98154 detected in mouse EST Accession BG083593.1.

[25609] SEQ ID:98155 detected in mouse EST Accession
AA756210.1.

[25610] SEQ ID:98156 detected in mouse EST Accession
AA624596.1.

[25611] SEQ ID:98157 detected in mouse EST Accession
BI414655.1.

[25612] SEQ ID:98682 detected in mouse EST Accession
AA636285.1.

[25613] GAM1649 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1649 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25614] An enzyme complex designated DICER COMPLEX, dices the GAM1649 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1649 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1649 RNA is designated SEQ ID:3298, and is provided hereinbelow with reference to the sequence listing part.

[25615] GAM1649 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1649 target RNA, herein designated GAM TARGET RNA. GAM1649 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25616] GAM1649 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1649 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1649 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1649 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1649 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25617] The complementary binding of GAM1649 RNA, herein designated GAM RNA, to target binding sites on GAM1649 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1649 target RNA, herein designated GAM TARGET RNA, into GAM1649 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25618] It is appreciated that GAM1649 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1649 target genes. The mRNA of each one of this plurality of GAM1649 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1649 RNA, herein designated GAM RNA, and which when bound by GAM1649 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1649 target proteins.

[25619] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1649 gene, herein designated GAM GENE, on one or more GAM1649 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[25620] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1649 correlate with, and may be deduced from, the identity of the target genes which GAM1649 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25621] Nucleotide sequences of the GAM1649 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1649 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1649 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1649 are further described hereinbelow with reference to Table Table1.

[25622] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1649 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25623] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1650 (GAM1650) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[25624] GAM1650 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1650 was detected is described hereinabove with reference to Figs. 2–8.

[25625] GAM1650 gene, herein designated GAM GENE, and GAM1650 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25626] GAM1650 gene, herein designated GAM GENE, encodes a GAM1650 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1650 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1650 precursor RNA is designated SEQ ID:1623, and is provided hereinbelow with reference to the sequence listing part.

[25627] GAM1650 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1650 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25628] An enzyme complex designated DICER COMPLEX, dices the GAM1650 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1650 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1650 RNA is designated SEQ ID:3299, and is provided hereinbelow with reference to the sequence listing part.

[25629] GAM1650 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1650 target RNA, herein designated GAM TARGET RNA. GAM1650 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25630] GAM1650 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1650 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1650 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1650 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1650 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25631] The complementary binding of GAM1650 RNA, herein designated GAM RNA, to target binding sites on GAM1650 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1650 target RNA, herein designated GAM TARGET RNA, into GAM1650 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25632] It is appreciated that GAM1650 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1650 target genes. The mRNA of each one of this plurality of GAM1650 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1650 RNA, herein designated GAM RNA, and which when bound by GAM1650 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1650 target proteins.

[25633] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1650 gene, herein designated GAM GENE, on one or more GAM1650 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25634] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1650 correlate with, and may be deduced from, the identity of the target genes which GAM1650 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25635] Nucleotide sequences of the GAM1650 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1650 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1650 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1650 are further described hereinbelow with reference to Table Table1.

- [25636] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1650 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.
- [25637] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1651 (GAM1651) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [25638] GAM1651 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1651 was detected is described hereinabove with reference to Figs. 2-8.
- [25639] GAM1651 gene, herein designated GAM GENE, and GAM1651 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [25640] GAM1651 gene, herein designated GAM GENE, encodes a GAM1651 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1651 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1651 precursor RNA is designated SEQ ID:1624, and is provided hereinbelow with reference to the sequence listing part.

[25641] GAM1651 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1651 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25642] An enzyme complex designated DICER COMPLEX, dices the GAM1651 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1651 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1651 RNA is designated SEQ ID:3300, and is provided hereinbelow with reference to the sequence listing part.

[25643] GAM1651 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1651 target RNA, herein designated GAM TARGET RNA. GAM1651 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25644] GAM1651 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1651 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1651 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1651 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1651 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25645] The complementary binding of GAM1651 RNA, herein designated GAM RNA, to target binding sites on GAM1651 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1651 target RNA, herein designated GAM TARGET RNA, into GAM1651 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25646] It is appreciated that GAM1651 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1651 target genes. The mRNA of each one of this plurality of GAM1651 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1651 RNA, herein designated GAM RNA, and which when bound by GAM1651 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1651 target proteins.

[25647] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1651 gene, herein designated GAM GENE, on one or more GAM1651 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25648] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1651 correlate with, and may

be deduced from, the identity of the target genes which GAM1651 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25649] Nucleotide sequences of the GAM1651 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1651 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1651 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1651 are further described hereinbelow with reference to Table Table1.

[25650] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1651 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25651] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1652 (GAM1652) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25652] GAM1652 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1652 was detected is described hereinabove with reference to Figs. 2-8.

[25653] GAM1652 gene, herein designated GAM GENE, and GAM1652 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25654] GAM1652 gene, herein designated GAM GENE, encodes a GAM1652 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1652 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1652 precursor RNA is designated SEQ ID:1625, and is provided hereinbelow with reference to the sequence listing part.

[25655] GAM1652 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1652 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25656] An enzyme complex designated DICER COMPLEX, dices the GAM1652 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1652 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1652 RNA is designated SEQ ID:3301, and is provided hereinbelow with reference to the sequence listing part.

[25657] GAM1652 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1652 target RNA, herein designated GAM TARGET RNA. GAM1652 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25658] GAM1652 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1652 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1652 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1652 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1652 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25659] The complementary binding of GAM1652 RNA, herein designated GAM RNA, to target binding sites on GAM1652 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1652 target RNA, herein designated GAM TARGET RNA, into GAM1652 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25660] It is appreciated that GAM1652 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1652 target genes. The mRNA of each one of this plurality of GAM1652 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1652 RNA, herein designated GAM RNA, and which when bound by GAM1652 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1652 target proteins.

[25661] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1652 gene, herein designated GAM GENE, on one or more GAM1652 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25662] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1652 correlate with, and may be deduced from, the identity of the target genes which GAM1652 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25663] Nucleotide sequences of the GAM1652 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1652 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1652 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1652 are further described hereinbelow with reference to Table Table1.

[25664] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1652 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[25665] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1653 (GAM1653) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25666] GAM1653 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1653 was detected is described hereinabove with reference to Figs. 2-8.

[25667] GAM1653 gene, herein designated GAM GENE, and GAM1653 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25668] GAM1653 gene, herein designated GAM GENE, encodes a GAM1653 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1653 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1653 precursor RNA is

designated SEQ ID:1626, and is provided hereinbelow with reference to the sequence listing part.

[25669] GAM1653 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1653 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25670] An enzyme complex designated DICER COMPLEX, dices the GAM1653 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1653 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1653 RNA is designated SEQ ID:3302, and is provided hereinbelow with reference to the sequence

listing part.

- [25671] GAM1653 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1653 target RNA, herein designated GAM TARGET RNA. GAM1653 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [25672] GAM1653 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1653 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1653 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1653 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1653 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25673] The complementary binding of GAM1653 RNA, herein designated GAM RNA, to target binding sites on GAM1653 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1653 target RNA, herein designated GAM TARGET RNA, into GAM1653 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25674] It is appreciated that GAM1653 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1653 target genes. The mRNA of each one of this plurality of GAM1653 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1653 RNA, herein designated GAM RNA, and which when bound by GAM1653 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1653 target proteins.

[25675] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1653 gene, herein designated GAM GENE, on one or more GAM1653 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25676] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1653 correlate with, and may be deduced from, the identity of the target genes which GAM1653 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25677] Nucleotide sequences of the GAM1653 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1653 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1653 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1653 are further described hereinbelow with reference to Table Table1.

[25678] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1653 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25679] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1654 (GAM1654) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25680] GAM1654 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1654 was detected is described hereinabove with reference to Figs. 2-8.

[25681] GAM1654 gene, herein designated GAM GENE, and GAM1654 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25682] GAM1654 gene, herein designated GAM GENE, encodes a GAM1654 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1654 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1654 precursor RNA is designated SEQ ID:1627, and is provided hereinbelow with reference to the sequence listing part.

[25683] GAM1654 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1654 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25684] An enzyme complex designated DICER COMPLEX, dices

the GAM1654 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1654 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1654 RNA is designated SEQ ID:3303, and is provided hereinbelow with reference to the sequence listing part.

[25685] GAM1654 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1654 target RNA, herein designated GAM TARGET RNA. GAM1654 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25686] GAM1654 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1654 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1654 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1654 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1654 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25687] The complementary binding of GAM1654 RNA, herein designated GAM RNA, to target binding sites on GAM1654 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1654 target RNA, herein designated GAM TARGET RNA, into GAM1654 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25688] It is appreciated that GAM1654 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1654 target genes. The mRNA of each one of this plurality of GAM1654 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1654 RNA, herein designated GAM RNA, and which when bound by GAM1654 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1654 target proteins.

[25689] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1654 gene, herein designated GAM GENE, on one or more GAM1654 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25690] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1654 correlate with, and may be deduced from, the identity of the target genes which GAM1654 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25691] Nucleotide sequences of the GAM1654 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1654 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1654 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1654 are further described hereinbelow with reference to Table Table1.

[25692] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1654 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25693] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1655 (GAM1655) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25694] GAM1655 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1655 was detected is described hereinabove with reference to Figs. 2-8.

[25695] GAM1655 gene, herein designated GAM GENE, and GAM1655 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25696] GAM1655 gene, herein designated GAM GENE, encodes a GAM1655 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1655 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1655 precursor RNA is designated SEQ ID:1628, and is provided hereinbelow with reference to the sequence listing part.

[25697] GAM1655 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1655 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25698] An enzyme complex designated DICER COMPLEX, dices the GAM1655 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1655 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1655 RNA is designated SEQ ID:3304, and is provided hereinbelow with reference to the sequence listing part.

[25699] GAM1655 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1655 target RNA, herein designated GAM TARGET RNA. GAM1655 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25700] GAM1655 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1655 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1655 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1655 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1655 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25701] The complementary binding of GAM1655 RNA, herein designated GAM RNA, to target binding sites on GAM1655 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1655 target RNA, herein designated GAM TARGET RNA, into GAM1655 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25702] It is appreciated that GAM1655 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1655 target genes. The mRNA of each one of this plurality of GAM1655 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1655 RNA, herein designated GAM RNA, and which when bound by GAM1655 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1655 target proteins.

[25703] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1655 gene, herein designated GAM GENE, on one or more GAM1655 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25704] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1655 correlate with, and may be deduced from, the identity of the target genes which GAM1655 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25705] Nucleotide sequences of the GAM1655 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1655 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1655 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1655 are further described hereinbelow with reference to Table Table1.

[25706] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1655 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25707] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1656 (GAM1656) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25708] GAM1656 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1656 was detected is described hereinabove with reference to Figs. 2-8.

[25709] GAM1656 gene, herein designated GAM GENE, and GAM1656 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25710] GAM1656 gene, herein designated GAM GENE, encodes a GAM1656 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1656 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1656 precursor RNA is designated SEQ ID:1629, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1629 is located at position 4851350 relative to contig NT_022517.13, on chromosome 3.

[25711] GAM1656 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1656 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25712] An enzyme complex designated DICER COMPLEX, dices the GAM1656 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1656 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1656 RNA is designated SEQ ID:3305, and is provided hereinbelow with reference to the sequence listing part.

[25713] GAM1656 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1656 target RNA, herein designated GAM TARGET RNA. GAM1656 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25714] GAM1656 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1656 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1656

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1656 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1656 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25715] The complementary binding of GAM1656 RNA, herein designated GAM RNA, to target binding sites on GAM1656 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1656 target RNA, herein designated GAM TARGET RNA, into GAM1656 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[25716] It is appreciated that GAM1656 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1656 target genes. The mRNA of each one of this plurality of GAM1656 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1656 RNA, herein designated GAM RNA, and which when bound by GAM1656 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1656 target proteins.

[25717] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1656 gene, herein designated GAM GENE, on one or more GAM1656 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25718] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1656 correlate with, and may be deduced from, the identity of the target genes which GAM1656 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25719] Nucleotide sequences of the GAM1656 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1656 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1656 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1656 are further described hereinbelow with reference to Table Table1.

[25720] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1656 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25721] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1657 (GAM1657) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25722] GAM1657 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1657 was detected is described hereinabove with reference to Figs. 2-8.

[25723] GAM1657 gene, herein designated GAM GENE, and GAM1657 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25724] GAM1657 gene, herein designated GAM GENE, encodes a GAM1657 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1657 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1657 precursor RNA is designated SEQ ID:1630, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1630 is located at position 33703762 relative to contig NT_007592.11, on chromosome 6.

[25725] GAM1657 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1657 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25726] An enzyme complex designated DICER COMPLEX, dices the GAM1657 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1657 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1657 RNA is designated SEQ ID:3306, and is provided hereinbelow with reference to the sequence listing part.

[25727] GAM1657 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM1657 target RNA, herein designated GAM TARGET RNA. GAM1657 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25728] GAM1657 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1657 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1657 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1657 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1657 target RNA, herein designated GAM TARGET

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25729] The complementary binding of GAM1657 RNA, herein designated GAM RNA, to target binding sites on GAM1657 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1657 target RNA, herein designated GAM TARGET RNA, into GAM1657 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25730] It is appreciated that GAM1657 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1657 target genes. The mRNA of each one of this plurality of GAM1657 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1657 RNA, herein designated GAM RNA, and which when bound by GAM1657 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1657 target proteins.

[25731] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1657 gene, herein designated GAM GENE, on one or more GAM1657 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25732] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1657 correlate with, and may be deduced from, the identity of the target genes which GAM1657 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25733] Nucleotide sequences of the GAM1657 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM1657 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1657 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1657 are further described hereinbelow with reference to Table Table1.

[25734] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1657 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25735] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1658 (GAM1658) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25736] GAM1658 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1658 was detected is described hereinabove with reference to Figs. 2-8.

[25737] GAM1658 gene, herein designated GAM GENE, and GAM1658 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[25738] GAM1658 gene, herein designated GAM GENE, encodes a GAM1658 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1658 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1658 precursor RNA is designated SEQ ID:1631, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1631 is located at position 180066 relative to contig NT_010859.10, on chromosome 18.

[25739] GAM1658 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1658 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25740] An enzyme complex designated DICER COMPLEX, dices

the GAM1658 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1658 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1658 RNA is designated SEQ ID:3307, and is provided hereinbelow with reference to the sequence listing part.

[25741] GAM1658 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1658 target RNA, herein designated GAM TARGET RNA. GAM1658 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25742] GAM1658 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1658 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1658 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1658 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1658 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25743] The complementary binding of GAM1658 RNA, herein designated GAM RNA, to target binding sites on GAM1658 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1658 target RNA, herein designated GAM TARGET RNA, into GAM1658 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25744] It is appreciated that GAM1658 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1658 target genes. The mRNA of each one of this plurality of GAM1658 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1658 RNA, herein designated GAM RNA, and which when bound by GAM1658 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1658 target proteins.

[25745] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1658 gene, herein designated GAM GENE, on one or more GAM1658 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25746] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1658 correlate with, and may be deduced from, the identity of the target genes which GAM1658 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25747] Nucleotide sequences of the GAM1658 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1658 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1658 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1658 are further described hereinbelow with reference to Table Table1.

[25748] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1658 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25749] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1659 (GAM1659) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25750] GAM1659 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1659 was detected is described hereinabove with reference to Figs. 2-8.

[25751] GAM1659 gene, herein designated GAM GENE, and GAM1659 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25752] GAM1659 gene, herein designated GAM GENE, encodes a GAM1659 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1659 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1659 precursor RNA is designated SEQ ID:1632, and is provided hereinbelow with reference to the sequence listing part.

[25753] GAM1659 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1659 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25754] An enzyme complex designated DICER COMPLEX, dices the GAM1659 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1659 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1659 RNA is designated SEQ ID:3308, and is provided hereinbelow with reference to the sequence listing part.

[25755] GAM1659 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1659 target RNA, herein designated GAM TARGET RNA. GAM1659 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25756] GAM1659 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1659 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1659 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1659 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1659 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25757] The complementary binding of GAM1659 RNA, herein designated GAM RNA, to target binding sites on GAM1659 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1659 target RNA, herein designated GAM TARGET RNA, into GAM1659 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25758] It is appreciated that GAM1659 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1659 target genes. The mRNA of each one of this plurality of GAM1659 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1659 RNA, herein designated GAM RNA, and which when bound by GAM1659 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1659 target proteins.

[25759] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1659 gene, herein designated GAM GENE, on one or more GAM1659 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25760] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1659 correlate with, and may be deduced from, the identity of the target genes which GAM1659 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25761] Nucleotide sequences of the GAM1659 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1659 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1659 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1659 are further described hereinbelow with reference to Table Table1.

[25762] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1659 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25763] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1660 (GAM1660) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25764] GAM1660 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1660 was detected is described hereinabove with reference to Figs. 2-8.

[25765] GAM1660 gene, herein designated GAM GENE, and GAM1660 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25766] GAM1660 gene, herein designated GAM GENE, encodes a GAM1660 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1660 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1660 precursor RNA is designated SEQ ID:1633, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1633 is located at position 28903785 relative to contig NT_007592.11, on chromosome 6.

[25767] GAM1660 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1660 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25768] An enzyme complex designated DICER COMPLEX, dices the GAM1660 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1660 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1660 RNA is designated SEQ ID:3309, and is provided hereinbelow with reference to the sequence listing part.

[25769] GAM1660 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1660 target RNA, herein designated GAM TARGET RNA. GAM1660 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25770] GAM1660 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1660 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1660

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1660 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1660 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25771] The complementary binding of GAM1660 RNA, herein designated GAM RNA, to target binding sites on GAM1660 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1660 target RNA, herein designated GAM TARGET RNA, into GAM1660 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[25772] It is appreciated that GAM1660 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1660 target genes. The mRNA of each one of this plurality of GAM1660 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1660 RNA, herein designated GAM RNA, and which when bound by GAM1660 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1660 target proteins.

[25773] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1660 gene, herein designated GAM GENE, on one or more GAM1660 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25774] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1660 correlate with, and may be deduced from, the identity of the target genes which GAM1660 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25775] Nucleotide sequences of the GAM1660 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1660 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1660 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1660 are further described hereinbelow with reference to Table Table1.

[25776] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1660 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25777] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1661 (GAM1661) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25778] GAM1661 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1661 was detected is described hereinabove with reference to Figs. 2-8.

[25779] GAM1661 gene, herein designated GAM GENE, and GAM1661 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25780] GAM1661 gene, herein designated GAM GENE, encodes a GAM1661 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1661 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1661 precursor RNA is designated SEQ ID:1634, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1634 is located at position 22191257 relative to contig NT_007299.11, on chromosome 6.

[25781] GAM1661 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1661 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25782] An enzyme complex designated DICER COMPLEX, dices the GAM1661 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1661 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1661 RNA is designated SEQ ID:3310, and is provided hereinbelow with reference to the sequence listing part.

[25783] GAM1661 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM1661 target RNA, herein designated GAM TARGET RNA. GAM1661 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25784] GAM1661 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1661 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1661 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1661 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1661 target RNA, herein designated GAM TARGET

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25785] The complementary binding of GAM1661 RNA, herein designated GAM RNA, to target binding sites on GAM1661 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1661 target RNA, herein designated GAM TARGET RNA, into GAM1661 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25786] It is appreciated that GAM1661 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1661 target genes. The mRNA of each one of this plurality of GAM1661 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1661 RNA, herein designated GAM RNA, and which when bound by GAM1661 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1661 target proteins.

[25787] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1661 gene, herein designated GAM GENE, on one or more GAM1661 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25788] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1661 correlate with, and may be deduced from, the identity of the target genes which GAM1661 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25789] Nucleotide sequences of the GAM1661 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM1661 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1661 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1661 are further described hereinbelow with reference to Table Table1.

[25790] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1661 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25791] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1662 (GAM1662) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25792] GAM1662 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1662 was detected is described hereinabove with reference to Figs. 2-8.

[25793] GAM1662 gene, herein designated GAM GENE, and GAM1662 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[25794] GAM1662 gene, herein designated GAM GENE, encodes a GAM1662 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1662 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1662 precursor RNA is designated SEQ ID:1635, and is provided hereinbelow with reference to the sequence listing part.

[25795] GAM1662 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1662 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25796] An enzyme complex designated DICER COMPLEX, dices the GAM1662 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1662 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1662 RNA is designated SEQ ID:3311, and is provided hereinbelow with reference to the sequence listing part.

[25797] GAM1662 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1662 target RNA, herein designated GAM TARGET RNA. GAM1662 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25798] GAM1662 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1662 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1662 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1662 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1662 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25799] The complementary binding of GAM1662 RNA, herein designated GAM RNA, to target binding sites on GAM1662 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1662 target RNA, herein designated GAM TARGET RNA, into GAM1662 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25800] It is appreciated that GAM1662 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1662 target genes. The mRNA of each one of this plurality of GAM1662 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1662 RNA, herein designated GAM RNA, and which when bound by GAM1662 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1662 target proteins.

[25801] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1662 gene, herein designated GAM GENE, on one or more GAM1662 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25802] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1662 correlate with, and may be deduced from, the identity of the target genes which GAM1662 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25803] Nucleotide sequences of the GAM1662 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1662 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1662 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1662 are further described hereinbelow with reference to Table Table1.

[25804] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1662 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25805] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1663 (GAM1663) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25806] GAM1663 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1663 was detected is described hereinabove with reference to Figs. 2-8.

[25807] GAM1663 gene, herein designated GAM GENE, and GAM1663 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25808] GAM1663 gene, herein designated GAM GENE, encodes a GAM1663 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1663 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1663 precursor RNA is designated SEQ ID:1636, and is provided hereinbelow with reference to the sequence listing part.

[25809] GAM1663 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1663 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25810] An enzyme complex designated DICER COMPLEX, dices the GAM1663 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1663 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1663 RNA is designated SEQ ID:3312, and is provided hereinbelow with reference to the sequence listing part.

[25811] GAM1663 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1663 target RNA, herein designated GAM TARGET RNA. GAM1663 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25812] GAM1663 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1663 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1663 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1663 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1663 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25813] The complementary binding of GAM1663 RNA, herein designated GAM RNA, to target binding sites on GAM1663 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1663 target RNA, herein designated GAM TARGET RNA, into GAM1663 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25814] It is appreciated that GAM1663 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1663 target genes. The mRNA of each one of this plurality of GAM1663 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1663 RNA, herein designated GAM RNA, and which when bound by GAM1663 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1663 target proteins.

[25815] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1663 gene, herein designated GAM GENE, on one or more GAM1663 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25816] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1663 correlate with, and may be deduced from, the identity of the target genes which GAM1663 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25817] Nucleotide sequences of the GAM1663 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1663 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1663 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1663 are further described hereinbelow with reference to Table Table1.

[25818] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1663 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25819] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1664 (GAM1664) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25820] GAM1664 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1664 was detected is described hereinabove with reference to Figs. 2-8.

[25821] GAM1664 gene, herein designated GAM GENE, and GAM1664 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25822] GAM1664 gene, herein designated GAM GENE, encodes a GAM1664 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1664 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1664 precursor RNA is designated SEQ ID:1637, and is provided hereinbelow with reference to the sequence listing part.

[25823] GAM1664 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:97948, which mouse homolog is detected in mouse EST accession AW475179.1.

[25824] GAM1664 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1664 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25825] An enzyme complex designated DICER COMPLEX, dices

the GAM1664 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1664 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1664 RNA is designated SEQ ID:3313, and is provided hereinbelow with reference to the sequence listing part.

[25826] GAM1664 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1664 target RNA, herein designated GAM TARGET RNA. GAM1664 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25827] GAM1664 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1664 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1664 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1664 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1664 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25828] The complementary binding of GAM1664 RNA, herein designated GAM RNA, to target binding sites on GAM1664 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1664 target RNA, herein designated GAM TARGET RNA, into GAM1664 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25829] It is appreciated that GAM1664 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1664 target genes. The mRNA of each one of this plurality of GAM1664 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1664 RNA, herein designated GAM RNA, and which when bound by GAM1664 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1664 target proteins.

[25830] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1664 gene, herein designated GAM GENE, on one or more GAM1664 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25831] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1664 correlate with, and may be deduced from, the identity of the target genes which GAM1664 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25832] Nucleotide sequences of the GAM1664 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1664 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1664 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1664 are further described hereinbelow with reference to Table Table1.

[25833] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1664 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25834] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1665 (GAM1665) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25835] GAM1665 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1665 was detected is described hereinabove with reference to Figs. 2-8.

[25836] GAM1665 gene, herein designated GAM GENE, and GAM1665 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25837] GAM1665 gene, herein designated GAM GENE, encodes a GAM1665 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1665 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1665 precursor RNA is designated SEQ ID:1638, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1638 is located at position 2349674 rela-

tive to contig NT_021907.13, on chromosome 1.

[25838] GAM1665 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1665 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25839] An enzyme complex designated DICER COMPLEX, dices the GAM1665 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1665 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1665 RNA is designated SEQ ID:3314, and is provided hereinbelow with reference to the sequence listing part.

[25840] GAM1665 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1665 target RNA, herein designated GAM TARGET RNA. GAM1665 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25841] GAM1665 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1665 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1665 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1665 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a

GAM1665 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25842] The complementary binding of GAM1665 RNA, herein designated GAM RNA, to target binding sites on GAM1665 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1665 target RNA, herein designated GAM TARGET RNA, into GAM1665 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25843] It is appreciated that GAM1665 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1665 target genes. The mRNA of each one of this plurality of GAM1665 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1665 RNA, herein designated GAM RNA, and which when bound by GAM1665 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1665

target proteins.

[25844] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1665 gene, herein designated GAM GENE, on one or more GAM1665 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25845] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1665 correlate with, and may be deduced from, the identity of the target genes which GAM1665 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25846] Nucleotide sequences of the GAM1665 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM1665 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1665 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1665 are further described hereinbelow with reference to Table Table1.

[25847] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1665 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25848] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1666 (GAM1666) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25849] GAM1666 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1666 was detected is described hereinabove with reference to Figs. 2-8.

[25850] GAM1666 gene, herein designated GAM GENE, and

GAM1666 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25851] GAM1666 gene, herein designated GAM GENE, encodes a GAM1666 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1666 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1666 precursor RNA is designated SEQ ID:1639, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1639 is located at position 3434852 relative to contig NT_009714.13, on chromosome 12.

[25852] GAM1666 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:97973, which mouse homolog is detected in mouse EST accession BG288438.1.

[25853] GAM1666 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1666 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25854] An enzyme complex designated DICER COMPLEX, dices the GAM1666 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1666 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1666 RNA is designated SEQ ID:3315, and is provided hereinbelow with reference to the sequence listing part.

[25855] GAM1666 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1666 target RNA, herein designated GAM TARGET RNA. GAM1666 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25856] GAM1666 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1666 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1666 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1666 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1666 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25857] The complementary binding of GAM1666 RNA, herein designated GAM RNA, to target binding sites on GAM1666 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1666 target RNA, herein designated GAM TARGET RNA, into GAM1666 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25858] It is appreciated that GAM1666 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1666 target genes. The mRNA of each one of this plurality of GAM1666 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1666 RNA, herein designated GAM RNA, and which when bound by GAM1666 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1666 target proteins.

[25859] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1666 gene, herein designated GAM GENE, on one or more GAM1666 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25860] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1666 correlate with, and may be deduced from, the identity of the target genes which GAM1666 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25861] Nucleotide sequences of the GAM1666 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1666 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1666 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1666 are further described hereinbelow with reference to Table Table1.

[25862] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1666 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25863] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1667 (GAM1667) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25864] GAM1667 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1667 was detected is described hereinabove with reference to Figs. 2-8.

[25865] GAM1667 gene, herein designated GAM GENE, and GAM1667 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25866] GAM1667 gene, herein designated GAM GENE, encodes a GAM1667 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1667 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1667 precursor RNA is designated SEQ ID:1640, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1640 is located at position 1259555 relative to contig NT_025965.9, on chromosome X.

[25867] GAM1667 has 7 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[25868] SEQ ID:99543 detected in mouse EST Accession AI098543.1.

[25869] SEQ ID:98077 detected in mouse EST Accession BG807367.1.

[25870] SEQ ID:98078 detected in mouse EST Accession BG915676.1.

[25871] SEQ ID:98079 detected in mouse EST Accession AI115901.1.

[25872] SEQ ID:98080 detected in mouse EST Accession BE371710.1.

[25873] SEQ ID:98083 detected in mouse EST Accession

BI788766.1.

[25874] SEQ ID:98084 detected in mouse EST Accession

BI789775.1.

[25875] GAM1667 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1667 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25876] An enzyme complex designated DICER COMPLEX, dices the GAM1667 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1667 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1667 RNA is designated SEQ ID:3316, and

is provided hereinbelow with reference to the sequence listing part.

[25877] GAM1667 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1667 target RNA, herein designated GAM TARGET RNA. GAM1667 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25878] GAM1667 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1667 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1667 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1667 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1667 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25879] The complementary binding of GAM1667 RNA, herein designated GAM RNA, to target binding sites on GAM1667 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1667 target RNA, herein designated GAM TARGET RNA, into GAM1667 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25880] It is appreciated that GAM1667 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1667 target genes. The mRNA of each one of this plurality of GAM1667 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1667 RNA, herein designated GAM RNA, and which when bound by

GAM1667 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1667 target proteins.

[25881] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1667 gene, herein designated GAM GENE, on one or more GAM1667 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25882] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1667 correlate with, and may be deduced from, the identity of the target genes which GAM1667 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

- [25883] Nucleotide sequences of the GAM1667 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1667 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1667 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1667 are further described hereinbelow with reference to Table Table1.
- [25884] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1667 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.
- [25885] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1668 (GAM1668) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [25886] GAM1668 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1668 was detected is described hereinabove

with reference to Figs. 2-8.

[25887] GAM1668 gene, herein designated GAM GENE, and GAM1668 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25888] GAM1668 gene, herein designated GAM GENE, encodes a GAM1668 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1668 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1668 precursor RNA is designated SEQ ID:1641, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1641 is located at position 1235091 relative to contig NT_009526.11, on chromosome 12.

[25889] GAM1668 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[25890] SEQ ID:100020 detected in mouse EST Accession AI326210.1.

[25891] SEQ ID:100021 detected in mouse EST Accession

BI965652.1.

[25892] SEQ ID:98851 detected in mouse EST Accession

BI965972.1.

[25893] GAM1668 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1668 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25894] An enzyme complex designated DICER COMPLEX, dices the GAM1668 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1668 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1668 RNA is designated SEQ ID:3317, and

is provided hereinbelow with reference to the sequence listing part.

[25895] GAM1668 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1668 target RNA, herein designated GAM TARGET RNA. GAM1668 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25896] GAM1668 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1668 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1668 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1668 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1668 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25897] The complementary binding of GAM1668 RNA, herein designated GAM RNA, to target binding sites on GAM1668 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1668 target RNA, herein designated GAM TARGET RNA, into GAM1668 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25898] It is appreciated that GAM1668 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1668 target genes. The mRNA of each one of this plurality of GAM1668 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1668 RNA, herein designated GAM RNA, and which when bound by

GAM1668 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1668 target proteins.

[25899] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1668 gene, herein designated GAM GENE, on one or more GAM1668 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25900] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1668 correlate with, and may be deduced from, the identity of the target genes which GAM1668 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

- [25901] Nucleotide sequences of the GAM1668 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1668 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1668 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1668 are further described hereinbelow with reference to Table Table1.
- [25902] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1668 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.
- [25903] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1669 (GAM1669) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [25904] GAM1669 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1669 was detected is described hereinabove

with reference to Figs. 2–8.

[25905] GAM1669 gene, herein designated GAM GENE, and GAM1669 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25906] GAM1669 gene, herein designated GAM GENE, encodes a GAM1669 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1669 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1669 precursor RNA is designated SEQ ID:1642, and is provided hereinbelow with reference to the sequence listing part.

[25907] GAM1669 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1669 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25908] An enzyme complex designated DICER COMPLEX, dices the GAM1669 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1669 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1669 RNA is designated SEQ ID:3318, and is provided hereinbelow with reference to the sequence listing part.

[25909] GAM1669 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1669 target RNA, herein designated GAM TARGET RNA. GAM1669 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25910] GAM1669 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1669 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1669 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1669 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1669 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25911] The complementary binding of GAM1669 RNA, herein designated GAM RNA, to target binding sites on GAM1669 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1669 target RNA, herein design-

nated GAM TARGET RNA, into GAM1669 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25912] It is appreciated that GAM1669 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1669 target genes. The mRNA of each one of this plurality of GAM1669 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1669 RNA, herein designated GAM RNA, and which when bound by GAM1669 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1669 target proteins.

[25913] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1669 gene, herein designated GAM GENE, on one or more GAM1669 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25914] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1669 correlate with, and may be deduced from, the identity of the target genes which GAM1669 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25915] Nucleotide sequences of the GAM1669 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1669 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1669 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1669 are further described hereinbelow with reference to Table Table1.

[25916] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1669 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[25917] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1670 (GAM1670) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25918] GAM1670 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1670 was detected is described hereinabove with reference to Figs. 2-8.

[25919] GAM1670 gene, herein designated GAM GENE, and GAM1670 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25920] GAM1670 gene, herein designated GAM GENE, encodes a GAM1670 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1670 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1670 precursor RNA is designated SEQ ID:1643, and is provided hereinbelow with reference to the sequence listing part. Nucleotide se-

quence SEQ ID:1643 is located at position 5677198 relative to contig NT_028309.8, on chromosome 11.

[25921] GAM1670 has 2 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[25922] SEQ ID:99535 detected in mouse EST Accession BI688569.1.

[25923] SEQ ID:99541 detected in mouse EST Accession BF021563.1.

[25924] GAM1670 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1670 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25925] An enzyme complex designated DICER COMPLEX, dices the GAM1670 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1670 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1670 RNA is designated SEQ ID:3319, and is provided hereinbelow with reference to the sequence listing part.

[25926] GAM1670 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1670 target RNA, herein designated GAM TARGET RNA. GAM1670 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25927] GAM1670 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1670 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1670

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1670 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1670 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25928] The complementary binding of GAM1670 RNA, herein designated GAM RNA, to target binding sites on GAM1670 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1670 target RNA, herein designated GAM TARGET RNA, into GAM1670 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[25929] It is appreciated that GAM1670 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1670 target genes. The mRNA of each one of this plurality of GAM1670 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1670 RNA, herein designated GAM RNA, and which when bound by GAM1670 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1670 target proteins.

[25930] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1670 gene, herein designated GAM GENE, on one or more GAM1670 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25931] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1670 correlate with, and may be deduced from, the identity of the target genes which GAM1670 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25932] Nucleotide sequences of the GAM1670 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1670 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1670 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1670 are further described hereinbelow with reference to Table Table1.

[25933] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1670 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25934] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1671 (GAM1671) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25935] GAM1671 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1671 was detected is described hereinabove with reference to Figs. 2-8.

[25936] GAM1671 gene, herein designated GAM GENE, and GAM1671 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25937] GAM1671 gene, herein designated GAM GENE, encodes a GAM1671 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1671 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1671 precursor RNA is designated SEQ ID:1644, and is provided hereinbelow with reference to the sequence listing part.

[25938] GAM1671 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1671 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25939] An enzyme complex designated DICER COMPLEX, dices the GAM1671 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1671 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1671 RNA is designated SEQ ID:3320, and is provided hereinbelow with reference to the sequence listing part.

[25940] GAM1671 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1671 target RNA, herein designated GAM TARGET

RNA. GAM1671 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25941] GAM1671 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1671 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1671 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1671 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1671 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25942] The complementary binding of GAM1671 RNA, herein designated GAM RNA, to target binding sites on GAM1671 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1671 target RNA, herein designated GAM TARGET RNA, into GAM1671 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25943] It is appreciated that GAM1671 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1671 target genes. The mRNA of each one of this plurality of GAM1671 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1671 RNA, herein designated GAM RNA, and which when bound by GAM1671 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1671 target proteins.

[25944] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1671 gene, herein designated GAM GENE, on one or more GAM1671 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25945] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1671 correlate with, and may be deduced from, the identity of the target genes which GAM1671 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25946] Nucleotide sequences of the GAM1671 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1671 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1671 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1671 are further described hereinbelow with reference to Table Table1.

[25947] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1671 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25948] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1672 (GAM1672) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25949] GAM1672 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1672 was detected is described hereinabove with reference to Figs. 2-8.

[25950] GAM1672 gene, herein designated GAM GENE, and GAM1672 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25951] GAM1672 gene, herein designated GAM GENE, encodes a

GAM1672 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1672 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1672 precursor RNA is designated SEQ ID:1645, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1645 is located at position 65229 relative to contig NT_024901.11, on chromosome 17.

[25952] GAM1672 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1672 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25953] An enzyme complex designated DICER COMPLEX, dices the GAM1672 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1672 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1672 RNA is designated SEQ ID:3321, and is provided hereinbelow with reference to the sequence listing part.

[25954] GAM1672 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1672 target RNA, herein designated GAM TARGET RNA. GAM1672 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25955] GAM1672 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1672 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1672 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1672 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1672 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25956] The complementary binding of GAM1672 RNA, herein designated GAM RNA, to target binding sites on GAM1672 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1672 target RNA, herein designated GAM TARGET RNA, into GAM1672 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25957] It is appreciated that GAM1672 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1672 target genes. The mRNA of each one of this plurality of GAM1672 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1672 RNA, herein designated GAM RNA, and which when bound by GAM1672 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1672 target proteins.

[25958] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1672 gene, herein designated GAM GENE, on one or more GAM1672 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25959] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1672 correlate with, and may be deduced from, the identity of the target genes which GAM1672 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25960] Nucleotide sequences of the GAM1672 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1672 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1672 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1672 are further described hereinbelow with reference to Table Table1.

[25961] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1672 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25962] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1673 (GAM1673) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25963] GAM1673 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1673 was detected is described hereinabove with reference to Figs. 2-8.

[25964] GAM1673 gene, herein designated GAM GENE, and GAM1673 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25965] GAM1673 gene, herein designated GAM GENE, encodes a GAM1673 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1673 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1673 precursor RNA is designated SEQ ID:1646, and is provided hereinbelow with reference to the sequence listing part.

[25966] GAM1673 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1673 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25967] An enzyme complex designated DICER COMPLEX, dices the GAM1673 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1673 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1673 RNA is designated SEQ ID:3322, and is provided hereinbelow with reference to the sequence listing part.

[25968] GAM1673 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1673 target RNA, herein designated GAM TARGET RNA. GAM1673 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25969] GAM1673 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1673 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1673 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1673 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1673 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25970] The complementary binding of GAM1673 RNA, herein designated GAM RNA, to target binding sites on GAM1673 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1673 target RNA, herein designated GAM TARGET RNA, into GAM1673 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25971] It is appreciated that GAM1673 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1673 target genes. The mRNA of each one of this plurality of GAM1673 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1673 RNA, herein designated GAM RNA, and which when bound by GAM1673 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1673 target proteins.

[25972] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1673 gene, herein designated GAM GENE, on one or more GAM1673 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25973] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1673 correlate with, and may be deduced from, the identity of the target genes which GAM1673 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25974] Nucleotide sequences of the GAM1673 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1673 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1673 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1673 are further described hereinbelow with reference to Table Table1.

[25975] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1673 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25976] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1674 (GAM1674) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25977] GAM1674 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1674 was detected is described hereinabove with reference to Figs. 2-8.

[25978] GAM1674 gene, herein designated GAM GENE, and GAM1674 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25979] GAM1674 gene, herein designated GAM GENE, encodes a GAM1674 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1674 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1674 precursor RNA is designated SEQ ID:1647, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1647 is located at position 365849 relative to contig NT_010799.11, on chromosome 17.

[25980] GAM1674 has 15 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[25981] SEQ ID:100065 detected in mouse EST Accession BG808025.1.

[25982] SEQ ID:100066 detected in mouse EST Accession BG808010.1.

[25983] SEQ ID:100067 detected in mouse EST Accession BG807850.1.

[25984] SEQ ID:100068 detected in mouse EST Accession BG805970.1.

[25985] SEQ ID:100127 detected in mouse EST Accession

AA671455.1.

[25986] SEQ ID:100128 detected in mouse EST Accession
AW824753.1.

[25987] SEQ ID:100129 detected in mouse EST Accession
BE943987.1.

[25988] SEQ ID:100130 detected in mouse EST Accession
BE691413.1.

[25989] SEQ ID:100131 detected in mouse EST Accession
BE691447.1.

[25990] SEQ ID:100132 detected in mouse EST Accession
AA144533.1.

[25991] SEQ ID:100133 detected in mouse EST Accession
BG145596.1.

[25992] SEQ ID:100134 detected in mouse EST Accession
BE692802.1.

[25993] SEQ ID:100135 detected in mouse EST Accession
AW208601.1.

[25994] SEQ ID:100136 detected in mouse EST Accession
BB610842.1.

[25995] SEQ ID:100137 detected in mouse EST Accession
BB609859.1.

[25996] GAM1674 precursor RNA, herein designated GAM PRE-
CURSOR RNA, folds onto itself, forming GAM1674 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25997] An enzyme complex designated DICER COMPLEX, dices the GAM1674 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1674 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1674 RNA is designated SEQ ID:3323, and is provided hereinbelow with reference to the sequence listing part.

[25998] GAM1674 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1674 target RNA, herein designated GAM TARGET

RNA. GAM1674 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25999] GAM1674 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1674 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1674 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1674 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1674 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26000] The complementary binding of GAM1674 RNA, herein designated GAM RNA, to target binding sites on GAM1674 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1674 target RNA, herein designated GAM TARGET RNA, into GAM1674 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26001] It is appreciated that GAM1674 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1674 target genes. The mRNA of each one of this plurality of GAM1674 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1674 RNA, herein designated GAM RNA, and which when bound by GAM1674 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1674 target proteins.

[26002] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1674 gene, herein designated GAM GENE, on one or more GAM1674 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26003] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1674 correlate with, and may be deduced from, the identity of the target genes which GAM1674 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26004] Nucleotide sequences of the GAM1674 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1674 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1674 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1674 are further described hereinbelow with reference to Table Table1.

[26005] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1674 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[26006] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1675 (GAM1675) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26007] GAM1675 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1675 was detected is described hereinabove with reference to Figs. 2-8.

[26008] GAM1675 gene, herein designated GAM GENE, and GAM1675 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[26009] GAM1675 gene, herein designated GAM GENE, encodes a

GAM1675 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1675 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1675 precursor RNA is designated SEQ ID:1648, and is provided hereinbelow with reference to the sequence listing part.

[26010] GAM1675 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1675 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26011] An enzyme complex designated DICER COMPLEX, dices the GAM1675 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1675 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1675 RNA is designated SEQ ID:3324, and is provided hereinbelow with reference to the sequence listing part.

[26012] GAM1675 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1675 target RNA, herein designated GAM TARGET RNA. GAM1675 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26013] GAM1675 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1675 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1675 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1675 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1675 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26014] The complementary binding of GAM1675 RNA, herein designated GAM RNA, to target binding sites on GAM1675 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1675 target RNA, herein designated GAM TARGET RNA, into GAM1675 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26015] It is appreciated that GAM1675 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1675 target genes. The mRNA of each one of this plurality of GAM1675 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1675 RNA, herein designated GAM RNA, and which when bound by GAM1675 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1675 target proteins.

[26016] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1675 gene, herein designated GAM GENE, on one or more GAM1675 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

- [26017] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1675 correlate with, and may be deduced from, the identity of the target genes which GAM1675 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.
- [26018] Nucleotide sequences of the GAM1675 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1675 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1675 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1675 are further described hereinbelow with reference to Table Table1.
- [26019] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1675 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.
- [26020] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1676 (GAM1676) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[26021] GAM1676 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1676 was detected is described hereinabove with reference to Figs. 2–8.

[26022] GAM1676 gene, herein designated GAM GENE, and GAM1676 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[26023] GAM1676 gene, herein designated GAM GENE, encodes a GAM1676 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1676 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1676 precursor RNA is designated SEQ ID:1649, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1649 is located at position 28311228 relative to contig NT_007819.11, on chromosome 7.

[26024] GAM1676 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1676 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26025] An enzyme complex designated DICER COMPLEX, dices the GAM1676 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1676 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1676 RNA is designated SEQ ID:3325, and is provided hereinbelow with reference to the sequence listing part.

[26026] GAM1676 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1676 target RNA, herein designated GAM TARGET RNA. GAM1676 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26027] GAM1676 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1676 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1676 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1676 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1676 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26028] The complementary binding of GAM1676 RNA, herein designated GAM RNA, to target binding sites on GAM1676 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1676 target RNA, herein designated GAM TARGET RNA, into GAM1676 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26029] It is appreciated that GAM1676 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1676 target genes. The mRNA of each one of this plurality of GAM1676 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1676 RNA, herein designated GAM RNA, and which when bound by GAM1676 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1676 target proteins.

[26030] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1676 gene, herein designated GAM GENE, on one or more GAM1676 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26031] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1676 correlate with, and may be deduced from, the identity of the target genes which GAM1676 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26032] Nucleotide sequences of the GAM1676 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1676 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1676 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1676 are further described hereinbelow with reference to Table Table1.

[26033] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1676 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[26034] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1677 (GAM1677) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26035] GAM1677 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1677 was detected is described hereinabove with reference to Figs. 2-8.

[26036] GAM1677 gene, herein designated GAM GENE, and GAM1677 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[26037] GAM1677 gene, herein designated GAM GENE, encodes a GAM1677 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1677 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1677 precursor RNA is designated SEQ ID:1650, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1650 is located at position 2183835 relative to contig NT_034383.2, on chromosome 1.

[26038] GAM1677 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1677 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26039] An enzyme complex designated DICER COMPLEX, dices the GAM1677 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1677 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1677 RNA is designated SEQ ID:3326, and is provided hereinbelow with reference to the sequence listing part.

[26040] GAM1677 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1677 target RNA, herein designated GAM TARGET RNA. GAM1677 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26041] GAM1677 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1677 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1677 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1677 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1677 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26042] The complementary binding of GAM1677 RNA, herein designated GAM RNA, to target binding sites on GAM1677 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1677 target RNA, herein designated GAM TARGET RNA, into GAM1677 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26043] It is appreciated that GAM1677 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1677 target genes. The mRNA of each one of this plurality of GAM1677 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1677 RNA, herein designated GAM RNA, and which when bound by GAM1677 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1677 target proteins.

[26044] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1677 gene, herein designated GAM GENE, on one or more GAM1677 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26045] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1677 correlate with, and may be deduced from, the identity of the target genes which GAM1677 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26046] Nucleotide sequences of the GAM1677 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1677 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1677 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1677 are further described hereinbelow with reference to Table Table1.

[26047] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1677 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[26048] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1678 (GAM1678) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26049] GAM1678 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1678 was detected is described hereinabove with reference to Figs. 2-8.

[26050] GAM1678 gene, herein designated GAM GENE, and GAM1678 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[26051] GAM1678 gene, herein designated GAM GENE, encodes a GAM1678 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1678 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1678 precursor RNA is designated SEQ ID:1651, and is provided hereinbelow with reference to the sequence listing part.

[26052] GAM1678 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1678 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26053] An enzyme complex designated DICER COMPLEX, dices the GAM1678 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1678 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1678 RNA is designated SEQ ID:3327, and is provided hereinbelow with reference to the sequence listing part.

[26054] GAM1678 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1678 target RNA, herein designated GAM TARGET RNA. GAM1678 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26055] GAM1678 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1678 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1678 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1678 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1678 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[26056] The complementary binding of GAM1678 RNA, herein designated GAM RNA, to target binding sites on GAM1678 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1678 target RNA, herein designated GAM TARGET RNA, into GAM1678 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26057] It is appreciated that GAM1678 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1678 target genes. The mRNA of each one of this plurality of GAM1678 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1678 RNA, herein designated GAM RNA, and which when bound by GAM1678 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1678 target proteins.

[26058] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1678 gene, herein designated GAM GENE, on one or

more GAM1678 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26059] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1678 correlate with, and may be deduced from, the identity of the target genes which GAM1678 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26060] Nucleotide sequences of the GAM1678 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1678 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1678 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1678 are further de-

scribed hereinbelow with reference to Table Table1.

[26061] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1678 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[26062] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1679 (GAM1679) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26063] GAM1679 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1679 was detected is described hereinabove with reference to Figs. 2-8.

[26064] GAM1679 gene, herein designated GAM GENE, and GAM1679 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[26065] GAM1679 gene, herein designated GAM GENE, encodes a GAM1679 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1679 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1679 precursor RNA is designated SEQ ID:1652, and is provided hereinbelow with reference to the sequence listing part.

[26066] GAM1679 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1679 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26067] An enzyme complex designated DICER COMPLEX, dices the GAM1679 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1679 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1679 RNA is designated SEQ ID:3328, and is provided hereinbelow with reference to the sequence listing part.

[26068] GAM1679 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1679 target RNA, herein designated GAM TARGET RNA. GAM1679 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26069] GAM1679 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1679 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1679 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1679 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1679 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26070] The complementary binding of GAM1679 RNA, herein designated GAM RNA, to target binding sites on GAM1679 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1679 target RNA, herein designated GAM TARGET RNA, into GAM1679 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26071] It is appreciated that GAM1679 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1679 target genes. The mRNA of each one of this plurality of GAM1679 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1679 RNA, herein designated GAM RNA, and which when bound by GAM1679 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1679 target proteins.

[26072] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1679 gene, herein designated GAM GENE, on one or more GAM1679 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26073] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1679 correlate with, and may be deduced from, the identity of the target genes which GAM1679 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26074] Nucleotide sequences of the GAM1679 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1679 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1679 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1679 are further described hereinbelow with reference to Table Table1.

[26075] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1679 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[26076] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1680 (GAM1680) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26077] GAM1680 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1680 was detected is described hereinabove with reference to Figs. 2-8.

[26078] GAM1680 gene, herein designated GAM GENE, and GAM1680 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[26079] GAM1680 gene, herein designated GAM GENE, encodes a GAM1680 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1680 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1680 precursor RNA is designated SEQ ID:1653, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1653 is located at position 4851359 relative to contig NT_022517.13, on chromosome 3.

[26080] GAM1680 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1680 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26081] An enzyme complex designated DICER COMPLEX, dices the GAM1680 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1680 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1680 RNA is designated SEQ ID:3329, and is provided hereinbelow with reference to the sequence listing part.

[26082] GAM1680 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1680 target RNA, herein designated GAM TARGET RNA. GAM1680 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26083] GAM1680 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1680 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1680 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1680 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1680 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26084] The complementary binding of GAM1680 RNA, herein designated GAM RNA, to target binding sites on GAM1680 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1680 target RNA, herein designated GAM TARGET RNA, into GAM1680 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26085] It is appreciated that GAM1680 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1680 target genes. The mRNA of each one of this plurality of GAM1680 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1680 RNA, herein designated GAM RNA, and which when bound by GAM1680 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1680 target proteins.

[26086] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1680 gene, herein designated GAM GENE, on one or more GAM1680 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26087] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1680 correlate with, and may be deduced from, the identity of the target genes which GAM1680 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26088] Nucleotide sequences of the GAM1680 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1680 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1680 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1680 are further described hereinbelow with reference to Table Table1.

[26089] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1680 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[26090] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1681 (GAM1681) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26091] GAM1681 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1681 was detected is described hereinabove with reference to Figs. 2-8.

[26092] GAM1681 gene, herein designated GAM GENE, and GAM1681 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[26093] GAM1681 gene, herein designated GAM GENE, encodes a GAM1681 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1681 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1681 precursor RNA is designated SEQ ID:1654, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1654 is located at position 4851359 relative to contig NT_022517.13, on chromosome 3.

[26094] GAM1681 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1681 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26095] An enzyme complex designated DICER COMPLEX, dices the GAM1681 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1681 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1681 RNA is designated SEQ ID:3330, and is provided hereinbelow with reference to the sequence listing part.

- [26096] GAM1681 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1681 target RNA, herein designated GAM TARGET RNA. GAM1681 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [26097] GAM1681 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1681 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1681 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1681 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1681 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26098] The complementary binding of GAM1681 RNA, herein designated GAM RNA, to target binding sites on GAM1681 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1681 target RNA, herein designated GAM TARGET RNA, into GAM1681 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26099] It is appreciated that GAM1681 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1681 target genes. The mRNA of each one of this

plurality of GAM1681 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1681 RNA, herein designated GAM RNA, and which when bound by GAM1681 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1681 target proteins.

[26100] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1681 gene, herein designated GAM GENE, on one or more GAM1681 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

- [26101] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1681 correlate with, and may be deduced from, the identity of the target genes which GAM1681 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.
- [26102] Nucleotide sequences of the GAM1681 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1681 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1681 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1681 are further described hereinbelow with reference to Table Table1.
- [26103] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1681 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.
- [26104] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1682 (GAM1682) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[26105] GAM1682 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1682 was detected is described hereinabove with reference to Figs. 2-8.

[26106] GAM1682 gene, herein designated GAM GENE, and GAM1682 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[26107] GAM1682 gene, herein designated GAM GENE, encodes a GAM1682 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1682 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1682 precursor RNA is designated SEQ ID:1655, and is provided hereinbelow with reference to the sequence listing part.

[26108] GAM1682 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1682 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26109] An enzyme complex designated DICER COMPLEX, dices the GAM1682 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1682 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1682 RNA is designated SEQ ID:3331, and is provided hereinbelow with reference to the sequence listing part.

[26110] GAM1682 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1682 target RNA, herein designated GAM TARGET RNA. GAM1682 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, design-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[26111] GAM1682 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1682 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1682 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1682 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1682 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26112] The complementary binding of GAM1682 RNA, herein

designated GAM RNA, to target binding sites on GAM1682 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1682 target RNA, herein designated GAM TARGET RNA, into GAM1682 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26113] It is appreciated that GAM1682 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1682 target genes. The mRNA of each one of this plurality of GAM1682 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1682 RNA, herein designated GAM RNA, and which when bound by GAM1682 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1682 target proteins.

[26114] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1682 gene, herein designated GAM GENE, on one or more GAM1682 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26115] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1682 correlate with, and may be deduced from, the identity of the target genes which GAM1682 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26116] Nucleotide sequences of the GAM1682 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1682 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1682 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1682 are further described hereinbelow with reference to Table Table1.

[26117] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1682 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[26118] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1683 (GAM1683) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26119] GAM1683 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1683 was detected is described hereinabove with reference to Figs. 2-8.

[26120] GAM1683 gene, herein designated GAM GENE, and GAM1683 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[26121] GAM1683 gene, herein designated GAM GENE, encodes a GAM1683 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1683 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1683 precursor RNA is designated SEQ ID:1656, and is provided hereinbelow with reference to the sequence listing part.

[26122] GAM1683 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1683 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26123] An enzyme complex designated DICER COMPLEX, dices the GAM1683 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1683 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1683 RNA is designated SEQ ID:3332, and is provided hereinbelow with reference to the sequence listing part.

[26124] GAM1683 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1683 target RNA, herein designated GAM TARGET RNA. GAM1683 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26125] GAM1683 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1683 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1683 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1683 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1683 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26126] The complementary binding of GAM1683 RNA, herein designated GAM RNA, to target binding sites on GAM1683 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1683 target RNA, herein designated GAM TARGET RNA, into GAM1683 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26127] It is appreciated that GAM1683 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1683 target genes. The mRNA of each one of this plurality of GAM1683 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1683 RNA,

herein designated GAM RNA, and which when bound by GAM1683 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1683 target proteins.

[26128] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1683 gene, herein designated GAM GENE, on one or more GAM1683 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26129] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1683 correlate with, and may be deduced from, the identity of the target genes which

GAM1683 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26130] Nucleotide sequences of the GAM1683 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1683 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1683 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1683 are further described hereinbelow with reference to Table Table1.

[26131] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1683 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[26132] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1684 (GAM1684) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26133] GAM1684 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1684 was detected is described hereinabove with reference to Figs. 2–8.

- [26134] GAM1684 gene, herein designated GAM GENE, and GAM1684 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [26135] GAM1684 gene, herein designated GAM GENE, encodes a GAM1684 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1684 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1684 precursor RNA is designated SEQ ID:1657, and is provided hereinbelow with reference to the sequence listing part.
- [26136] GAM1684 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1684 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[26137] An enzyme complex designated DICER COMPLEX, dices the GAM1684 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1684 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1684 RNA is designated SEQ ID:3333, and is provided hereinbelow with reference to the sequence listing part.

[26138] GAM1684 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1684 target RNA, herein designated GAM TARGET RNA. GAM1684 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26139] GAM1684 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1684 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1684 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1684 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1684 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26140] The complementary binding of GAM1684 RNA, herein designated GAM RNA, to target binding sites on GAM1684 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1684 target RNA, herein designated GAM TARGET RNA, into GAM1684 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26141] It is appreciated that GAM1684 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1684 target genes. The mRNA of each one of this plurality of GAM1684 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1684 RNA, herein designated GAM RNA, and which when bound by GAM1684 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1684 target proteins.

[26142] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1684 gene, herein designated GAM GENE, on one or more GAM1684 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26143] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1684 correlate with, and may be deduced from, the identity of the target genes which GAM1684 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26144] Nucleotide sequences of the GAM1684 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1684 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1684 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1684 are further described hereinbelow with reference to Table Table1.

[26145] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1684 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[26146] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1685 (GAM1685) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26147] GAM1685 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1685 was detected is described hereinabove with reference to Figs. 2-8.

[26148] GAM1685 gene, herein designated GAM GENE, and GAM1685 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[26149] GAM1685 gene, herein designated GAM GENE, encodes a GAM1685 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1685 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1685 precursor RNA is designated SEQ ID:1658, and is provided hereinbelow with

reference to the sequence listing part.

[26150] GAM1685 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1685 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26151] An enzyme complex designated DICER COMPLEX, dices the GAM1685 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1685 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1685 RNA is designated SEQ ID:3334, and is provided hereinbelow with reference to the sequence listing part.

[26152] GAM1685 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1685 target RNA, herein designated GAM TARGET RNA. GAM1685 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26153] GAM1685 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1685 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1685 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1685 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a

GAM1685 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26154] The complementary binding of GAM1685 RNA, herein designated GAM RNA, to target binding sites on GAM1685 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1685 target RNA, herein designated GAM TARGET RNA, into GAM1685 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26155] It is appreciated that GAM1685 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1685 target genes. The mRNA of each one of this plurality of GAM1685 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1685 RNA, herein designated GAM RNA, and which when bound by GAM1685 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1685

target proteins.

[26156] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1685 gene, herein designated GAM GENE, on one or more GAM1685 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26157] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1685 correlate with, and may be deduced from, the identity of the target genes which GAM1685 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26158] Nucleotide sequences of the GAM1685 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM1685 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1685 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1685 are further described hereinbelow with reference to Table Table1.

[26159] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1685 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[26160] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1686 (GAM1686) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26161] GAM1686 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1686 was detected is described hereinabove with reference to Figs. 2-8.

[26162] GAM1686 gene, herein designated GAM GENE, and

GAM1686 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[26163] GAM1686 gene, herein designated GAM GENE, encodes a GAM1686 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1686 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1686 precursor RNA is designated SEQ ID:1659, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1659 is located at position 387404 relative to contig NT_022508.11, on chromosome 3.

[26164] GAM1686 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1686 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26165] An enzyme complex designated DICER COMPLEX, dices the GAM1686 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1686 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1686 RNA is designated SEQ ID:3335, and is provided hereinbelow with reference to the sequence listing part.

[26166] GAM1686 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1686 target RNA, herein designated GAM TARGET RNA. GAM1686 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26167] GAM1686 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1686 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1686 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1686 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1686 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26168] The complementary binding of GAM1686 RNA, herein designated GAM RNA, to target binding sites on GAM1686 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1686 target RNA, herein design-

nated GAM TARGET RNA, into GAM1686 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26169] It is appreciated that GAM1686 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1686 target genes. The mRNA of each one of this plurality of GAM1686 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1686 RNA, herein designated GAM RNA, and which when bound by GAM1686 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1686 target proteins.

[26170] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1686 gene, herein designated GAM GENE, on one or more GAM1686 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26171] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1686 correlate with, and may be deduced from, the identity of the target genes which GAM1686 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26172] Nucleotide sequences of the GAM1686 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1686 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1686 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1686 are further described hereinbelow with reference to Table Table1.

[26173] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1686 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[26174] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1687 (GAM1687) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26175] GAM1687 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1687 was detected is described hereinabove with reference to Figs. 2-8.

[26176] GAM1687 gene, herein designated GAM GENE, and GAM1687 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[26177] GAM1687 gene, herein designated GAM GENE, encodes a GAM1687 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1687 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1687 precursor RNA is designated SEQ ID:1660, and is provided hereinbelow with reference to the sequence listing part. Nucleotide se-

quence SEQ ID:1660 is located at position 387404 relative to contig NT_022508.11, on chromosome 3.

[26178] GAM1687 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1687 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26179] An enzyme complex designated DICER COMPLEX, dices the GAM1687 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1687 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1687 RNA is designated SEQ ID:3336, and is provided hereinbelow with reference to the sequence

listing part.

- [26180] GAM1687 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1687 target RNA, herein designated GAM TARGET RNA. GAM1687 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [26181] GAM1687 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1687 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1687 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1687 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1687 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26182] The complementary binding of GAM1687 RNA, herein designated GAM RNA, to target binding sites on GAM1687 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1687 target RNA, herein designated GAM TARGET RNA, into GAM1687 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26183] It is appreciated that GAM1687 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1687 target genes. The mRNA of each one of this plurality of GAM1687 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1687 RNA, herein designated GAM RNA, and which when bound by GAM1687 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1687 target proteins.

[26184] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1687 gene, herein designated GAM GENE, on one or more GAM1687 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26185] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1687 correlate with, and may be deduced from, the identity of the target genes which GAM1687 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

- [26186] Nucleotide sequences of the GAM1687 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1687 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1687 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1687 are further described hereinbelow with reference to Table Table1.
- [26187] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1687 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.
- [26188] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1688 (GAM1688) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [26189] GAM1688 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1688 was detected is described hereinabove with reference to Figs. 2-8.

[26190] GAM1688 gene, herein designated GAM GENE, and GAM1688 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[26191] GAM1688 gene, herein designated GAM GENE, encodes a GAM1688 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1688 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1688 precursor RNA is designated SEQ ID:1661, and is provided hereinbelow with reference to the sequence listing part.

[26192] GAM1688 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1688 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26193] An enzyme complex designated DICER COMPLEX, dices

the GAM1688 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1688 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1688 RNA is designated SEQ ID:3337, and is provided hereinbelow with reference to the sequence listing part.

[26194] GAM1688 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1688 target RNA, herein designated GAM TARGET RNA. GAM1688 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26195] GAM1688 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1688 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1688 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1688 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1688 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26196] The complementary binding of GAM1688 RNA, herein designated GAM RNA, to target binding sites on GAM1688 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1688 target RNA, herein designated GAM TARGET RNA, into GAM1688 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26197] It is appreciated that GAM1688 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1688 target genes. The mRNA of each one of this plurality of GAM1688 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1688 RNA, herein designated GAM RNA, and which when bound by GAM1688 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1688 target proteins.

[26198] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1688 gene, herein designated GAM GENE, on one or more GAM1688 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26199] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1688 correlate with, and may be deduced from, the identity of the target genes which GAM1688 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26200] Nucleotide sequences of the GAM1688 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1688 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1688 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1688 are further described hereinbelow with reference to Table Table1.

[26201] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1688 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[26202] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1689 (GAM1689) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26203] GAM1689 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1689 was detected is described hereinabove with reference to Figs. 2-8.

[26204] GAM1689 gene, herein designated GAM GENE, and GAM1689 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[26205] GAM1689 gene, herein designated GAM GENE, encodes a GAM1689 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1689 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1689 precursor RNA is designated SEQ ID:1662, and is provided hereinbelow with reference to the sequence listing part.

[26206] GAM1689 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1689 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26207] An enzyme complex designated DICER COMPLEX, dices the GAM1689 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1689 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1689 RNA is designated SEQ ID:3338, and is provided hereinbelow with reference to the sequence listing part.

[26208] GAM1689 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1689 target RNA, herein designated GAM TARGET RNA. GAM1689 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26209] GAM1689 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1689 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1689 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1689 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1689 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26210] The complementary binding of GAM1689 RNA, herein designated GAM RNA, to target binding sites on GAM1689 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1689 target RNA, herein designated GAM TARGET RNA, into GAM1689 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26211] It is appreciated that GAM1689 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1689 target genes. The mRNA of each one of this plurality of GAM1689 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1689 RNA, herein designated GAM RNA, and which when bound by GAM1689 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1689 target proteins.

[26212] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1689 gene, herein designated GAM GENE, on one or more GAM1689 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26213] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1689 correlate with, and may be deduced from, the identity of the target genes which GAM1689 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26214] Nucleotide sequences of the GAM1689 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1689 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1689 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1689 are further described hereinbelow with reference to Table Table1.

[26215] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1689 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[26216] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1690 (GAM1690) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26217] GAM1690 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1690 was detected is described hereinabove with reference to Figs. 2-8.

[26218] GAM1690 gene, herein designated GAM GENE, and GAM1690 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[26219] GAM1690 gene, herein designated GAM GENE, encodes a GAM1690 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1690 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1690 precursor RNA is designated SEQ ID:1663, and is provided hereinbelow with reference to the sequence listing part.

[26220] GAM1690 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1690 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26221] An enzyme complex designated DICER COMPLEX, dices the GAM1690 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1690 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1690 RNA is designated SEQ ID:3339, and is provided hereinbelow with reference to the sequence listing part.

[26222] GAM1690 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1690 target RNA, herein designated GAM TARGET RNA. GAM1690 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26223] GAM1690 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1690 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1690 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1690 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1690 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26224] The complementary binding of GAM1690 RNA, herein designated GAM RNA, to target binding sites on GAM1690 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1690 target RNA, herein designated GAM TARGET RNA, into GAM1690 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26225] It is appreciated that GAM1690 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1690 target genes. The mRNA of each one of this plurality of GAM1690 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1690 RNA, herein designated GAM RNA, and which when bound by GAM1690 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1690 target proteins.

[26226] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1690 gene, herein designated GAM GENE, on one or more GAM1690 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26227] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1690 correlate with, and may be deduced from, the identity of the target genes which GAM1690 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26228] Nucleotide sequences of the GAM1690 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1690 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1690 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1690 are further described hereinbelow with reference to Table Table1.

[26229] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1690 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[26230] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1691 (GAM1691) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26231] GAM1691 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1691 was detected is described hereinabove with reference to Figs. 2-8.

[26232] GAM1691 gene, herein designated GAM GENE, and GAM1691 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[26233] GAM1691 gene, herein designated GAM GENE, encodes a GAM1691 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1691 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1691 precursor RNA is designated SEQ ID:1664, and is provided hereinbelow with reference to the sequence listing part.

[26234] GAM1691 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1691 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26235] An enzyme complex designated DICER COMPLEX, dices the GAM1691 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1691 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1691 RNA is designated SEQ ID:3340, and is provided hereinbelow with reference to the sequence listing part.

[26236] GAM1691 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1691 target RNA, herein designated GAM TARGET RNA. GAM1691 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26237] GAM1691 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1691 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1691 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1691 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1691 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[26238] The complementary binding of GAM1691 RNA, herein designated GAM RNA, to target binding sites on GAM1691 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1691 target RNA, herein designated GAM TARGET RNA, into GAM1691 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26239] It is appreciated that GAM1691 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1691 target genes. The mRNA of each one of this plurality of GAM1691 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1691 RNA, herein designated GAM RNA, and which when bound by GAM1691 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1691 target proteins.

[26240] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1691 gene, herein designated GAM GENE, on one or

more GAM1691 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26241] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1691 correlate with, and may be deduced from, the identity of the target genes which GAM1691 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26242] Nucleotide sequences of the GAM1691 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1691 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1691 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1691 are further de-

scribed hereinbelow with reference to Table Table1.

[26243] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1691 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[26244] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1692 (GAM1692) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26245] GAM1692 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1692 was detected is described hereinabove with reference to Figs. 2-8.

[26246] GAM1692 gene, herein designated GAM GENE, and GAM1692 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[26247] GAM1692 gene, herein designated GAM GENE, encodes a GAM1692 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1692 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1692 precursor RNA is designated SEQ ID:1665, and is provided hereinbelow with reference to the sequence listing part.

[26248] GAM1692 has 7 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[26249] SEQ ID:100000 detected in mouse EST Accession BF152625.1.

[26250] SEQ ID:100001 detected in mouse EST Accession AI614809.1.

[26251] SEQ ID:100002 detected in mouse EST Accession AA065653.1.

[26252] SEQ ID:100003 detected in mouse EST Accession AI153186.1.

[26253] SEQ ID:100004 detected in mouse EST Accession AW744693.1.

[26254] SEQ ID:100005 detected in mouse EST Accession BF101508.1.

[26255] SEQ ID:100006 detected in mouse EST Accession BG261697.1.

[26256] GAM1692 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1692 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26257] An enzyme complex designated DICER COMPLEX, dices the GAM1692 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1692 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1692 RNA is designated SEQ ID:3341, and is provided hereinbelow with reference to the sequence

listing part.

- [26258] GAM1692 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1692 target RNA, herein designated GAM TARGET RNA. GAM1692 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [26259] GAM1692 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1692 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1692 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1692 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1692 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26260] The complementary binding of GAM1692 RNA, herein designated GAM RNA, to target binding sites on GAM1692 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1692 target RNA, herein designated GAM TARGET RNA, into GAM1692 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26261] It is appreciated that GAM1692 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1692 target genes. The mRNA of each one of this plurality of GAM1692 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1692 RNA, herein designated GAM RNA, and which when bound by GAM1692 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1692 target proteins.

[26262] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1692 gene, herein designated GAM GENE, on one or more GAM1692 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26263] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1692 correlate with, and may be deduced from, the identity of the target genes which GAM1692 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26264] Nucleotide sequences of the GAM1692 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1692 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1692 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1692 are further described hereinbelow with reference to Table Table1.

[26265] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1692 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[26266] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1693 (GAM1693) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26267] GAM1693 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1693 was detected is described hereinabove with reference to Figs. 2-8.

[26268] GAM1693 gene, herein designated GAM GENE, and GAM1693 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[26269] GAM1693 gene, herein designated GAM GENE, encodes a GAM1693 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1693 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1693 precursor RNA is designated SEQ ID:1666, and is provided hereinbelow with reference to the sequence listing part.

[26270] GAM1693 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1693 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26271] An enzyme complex designated DICER COMPLEX, dices

the GAM1693 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1693 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1693 RNA is designated SEQ ID:3342, and is provided hereinbelow with reference to the sequence listing part.

[26272] GAM1693 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1693 target RNA, herein designated GAM TARGET RNA. GAM1693 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26273] GAM1693 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1693 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1693 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1693 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1693 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26274] The complementary binding of GAM1693 RNA, herein designated GAM RNA, to target binding sites on GAM1693 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1693 target RNA, herein designated GAM TARGET RNA, into GAM1693 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26275] It is appreciated that GAM1693 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1693 target genes. The mRNA of each one of this plurality of GAM1693 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1693 RNA, herein designated GAM RNA, and which when bound by GAM1693 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1693 target proteins.

[26276] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1693 gene, herein designated GAM GENE, on one or more GAM1693 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26277] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1693 correlate with, and may be deduced from, the identity of the target genes which GAM1693 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26278] Nucleotide sequences of the GAM1693 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1693 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1693 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1693 are further described hereinbelow with reference to Table Table1.

[26279] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1693 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[26280] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1694 (GAM1694) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26281] GAM1694 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1694 was detected is described hereinabove with reference to Figs. 2-8.

[26282] GAM1694 gene, herein designated GAM GENE, and GAM1694 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[26283] GAM1694 gene, herein designated GAM GENE, encodes a GAM1694 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1694 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1694 precursor RNA is designated SEQ ID:1667, and is provided hereinbelow with reference to the sequence listing part.

[26284] GAM1694 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1694 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26285] An enzyme complex designated DICER COMPLEX, dices the GAM1694 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1694 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1694 RNA is designated SEQ ID:3343, and is provided hereinbelow with reference to the sequence listing part.

[26286] GAM1694 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1694 target RNA, herein designated GAM TARGET RNA. GAM1694 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26287] GAM1694 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1694 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1694 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1694 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1694 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26288] The complementary binding of GAM1694 RNA, herein designated GAM RNA, to target binding sites on GAM1694 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1694 target RNA, herein designated GAM TARGET RNA, into GAM1694 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26289] It is appreciated that GAM1694 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1694 target genes. The mRNA of each one of this plurality of GAM1694 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1694 RNA, herein designated GAM RNA, and which when bound by GAM1694 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1694 target proteins.

[26290] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1694 gene, herein designated GAM GENE, on one or more GAM1694 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26291] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1694 correlate with, and may be deduced from, the identity of the target genes which GAM1694 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26292] Nucleotide sequences of the GAM1694 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1694 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1694 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1694 are further described hereinbelow with reference to Table Table1.

[26293] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1694 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[26294] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1695 (GAM1695) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26295] GAM1695 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1695 was detected is described hereinabove with reference to Figs. 2-8.

[26296] GAM1695 gene, herein designated GAM GENE, and GAM1695 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[26297] GAM1695 gene, herein designated GAM GENE, encodes a GAM1695 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1695 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1695 precursor RNA is designated SEQ ID:1668, and is provided hereinbelow with reference to the sequence listing part.

[26298] GAM1695 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1695 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26299] An enzyme complex designated DICER COMPLEX, dices the GAM1695 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1695 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1695 RNA is designated SEQ ID:3344, and is provided hereinbelow with reference to the sequence listing part.

[26300] GAM1695 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1695 target RNA, herein designated GAM TARGET RNA. GAM1695 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26301] GAM1695 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1695 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1695 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1695 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1695 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26302] The complementary binding of GAM1695 RNA, herein designated GAM RNA, to target binding sites on GAM1695 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1695 target RNA, herein designated GAM TARGET RNA, into GAM1695 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26303] It is appreciated that GAM1695 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1695 target genes. The mRNA of each one of this plurality of GAM1695 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1695 RNA, herein designated GAM RNA, and which when bound by GAM1695 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1695 target proteins.

[26304] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1695 gene, herein designated GAM GENE, on one or more GAM1695 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26305] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1695 correlate with, and may be deduced from, the identity of the target genes which GAM1695 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26306] Nucleotide sequences of the GAM1695 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1695 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1695 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1695 are further described hereinbelow with reference to Table Table1.

[26307] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1695 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[26308] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1696 (GAM1696) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26309] GAM1696 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1696 was detected is described hereinabove with reference to Figs. 2-8.

[26310] GAM1696 gene, herein designated GAM GENE, and GAM1696 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[26311] GAM1696 gene, herein designated GAM GENE, encodes a GAM1696 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1696 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1696 precursor RNA is designated SEQ ID:1669, and is provided hereinbelow with reference to the sequence listing part.

[26312] GAM1696 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1696 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26313] An enzyme complex designated DICER COMPLEX, dices the GAM1696 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1696 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1696 RNA is designated SEQ ID:3345, and is provided hereinbelow with reference to the sequence listing part.

[26314] GAM1696 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1696 target RNA, herein designated GAM TARGET RNA. GAM1696 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26315] GAM1696 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1696 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1696 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1696 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1696 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[26316] The complementary binding of GAM1696 RNA, herein designated GAM RNA, to target binding sites on GAM1696 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1696 target RNA, herein designated GAM TARGET RNA, into GAM1696 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26317] It is appreciated that GAM1696 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1696 target genes. The mRNA of each one of this plurality of GAM1696 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1696 RNA, herein designated GAM RNA, and which when bound by GAM1696 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1696 target proteins.

[26318] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1696 gene, herein designated GAM GENE, on one or

more GAM1696 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26319] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1696 correlate with, and may be deduced from, the identity of the target genes which GAM1696 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26320] Nucleotide sequences of the GAM1696 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1696 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1696 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1696 are further de-

scribed hereinbelow with reference to Table Table1.

[26321] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1696 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[26322] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1697 (GAM1697) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26323] GAM1697 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1697 was detected is described hereinabove with reference to Figs. 2-8.

[26324] GAM1697 gene, herein designated GAM GENE, and GAM1697 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[26325] GAM1697 gene, herein designated GAM GENE, encodes a GAM1697 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1697 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1697 precursor RNA is designated SEQ ID:1670, and is provided hereinbelow with reference to the sequence listing part.

[26326] GAM1697 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1697 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26327] An enzyme complex designated DICER COMPLEX, dices the GAM1697 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1697 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1697 RNA is designated SEQ ID:3346, and is provided hereinbelow with reference to the sequence listing part.

[26328] GAM1697 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1697 target RNA, herein designated GAM TARGET RNA. GAM1697 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26329] GAM1697 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1697 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1697 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1697 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1697 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26330] The complementary binding of GAM1697 RNA, herein designated GAM RNA, to target binding sites on GAM1697 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1697 target RNA, herein designated GAM TARGET RNA, into GAM1697 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26331] It is appreciated that GAM1697 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1697 target genes. The mRNA of each one of this plurality of GAM1697 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1697 RNA, herein designated GAM RNA, and which when bound by GAM1697 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1697 target proteins.

[26332] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1697 gene, herein designated GAM GENE, on one or more GAM1697 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26333] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1697 correlate with, and may be deduced from, the identity of the target genes which GAM1697 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26334] Nucleotide sequences of the GAM1697 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1697 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1697 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1697 are further described hereinbelow with reference to Table Table1.

[26335] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1697 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[26336] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1698 (GAM1698) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26337] GAM1698 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1698 was detected is described hereinabove with reference to Figs. 2-8.

[26338] GAM1698 gene, herein designated GAM GENE, and GAM1698 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[26339] GAM1698 gene, herein designated GAM GENE, encodes a GAM1698 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1698 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1698 precursor RNA is designated SEQ ID:1671, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1671 is located at position 1235063 relative to contig NT_009526.11, on chromosome 12.

[26340] GAM1698 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[26341] SEQ ID:100017 detected in mouse EST Accession
BI965972.1.

[26342] SEQ ID:100018 detected in mouse EST Accession
AI326210.1.

[26343] SEQ ID:100019 detected in mouse EST Accession
BI965652.1.

[26344] GAM1698 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1698 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26345] An enzyme complex designated DICER COMPLEX, dices the GAM1698 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1698 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1698 RNA is designated SEQ ID:3347, and is provided hereinbelow with reference to the sequence listing part.

[26346] GAM1698 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1698 target RNA, herein designated GAM TARGET RNA. GAM1698 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[26347] GAM1698 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1698 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1698 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1698 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1698 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26348] The complementary binding of GAM1698 RNA, herein designated GAM RNA, to target binding sites on GAM1698 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1698 target RNA, herein designated GAM TARGET RNA, into GAM1698 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26349] It is appreciated that GAM1698 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1698 target genes. The mRNA of each one of this plurality of GAM1698 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1698 RNA, herein designated GAM RNA, and which when bound by GAM1698 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1698 target proteins.

[26350] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1698 gene, herein designated GAM GENE, on one or more GAM1698 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26351] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1698 correlate with, and may be deduced from, the identity of the target genes which GAM1698 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26352] Nucleotide sequences of the GAM1698 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1698 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1698 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1698 are further described hereinbelow with reference to Table Table1.

[26353] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1698 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[26354] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1699 (GAM1699) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26355] GAM1699 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1699 was detected is described hereinabove with reference to Figs. 2-8.

[26356] GAM1699 gene, herein designated GAM GENE, and GAM1699 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[26357] GAM1699 gene, herein designated GAM GENE, encodes a GAM1699 precursor RNA, herein designated GAM PRE-CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1699 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1699 precursor RNA is designated SEQ ID:1672, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1672 is located at position 365814 relative to contig NT_010799.11, on chromosome 17.

[26358] GAM1699 has 15 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

- [26359] SEQ ID:97958 detected in mouse EST Accession
BE953126.1.
- [26360] SEQ ID:97959 detected in mouse EST Accession
AA144533.1.
- [26361] SEQ ID:97960 detected in mouse EST Accession
AA671455.1.
- [26362] SEQ ID:97961 detected in mouse EST Accession
AW824753.1.
- [26363] SEQ ID:97962 detected in mouse EST Accession
BE943987.1.
- [26364] SEQ ID:97963 detected in mouse EST Accession
BE691447.1.
- [26365] SEQ ID:97964 detected in mouse EST Accession
BG808025.1.
- [26366] SEQ ID:97965 detected in mouse EST Accession
BG808010.1.
- [26367] SEQ ID:97966 detected in mouse EST Accession
BG807850.1.
- [26368] SEQ ID:97967 detected in mouse EST Accession
BG805970.1.
- [26369] SEQ ID:97968 detected in mouse EST Accession
BG145596.1.
- [26370] SEQ ID:97969 detected in mouse EST Accession

AW208601.1.

[26371] SEQ ID:97970 detected in mouse EST Accession
BB609859.1.

[26372] SEQ ID:97971 detected in mouse EST Accession
BB610842.1.

[26373] SEQ ID:97972 detected in mouse EST Accession
BE691413.1.

[26374] GAM1699 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1699 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26375] An enzyme complex designated DICER COMPLEX, dices the GAM1699 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1699 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1699 RNA is designated SEQ ID:3348, and is provided hereinbelow with reference to the sequence listing part.

- [26376] GAM1699 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1699 target RNA, herein designated GAM TARGET RNA. GAM1699 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [26377] GAM1699 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1699 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1699 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1699 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1699 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[26378] The complementary binding of GAM1699 RNA, herein designated GAM RNA, to target binding sites on GAM1699 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1699 target RNA, herein designated GAM TARGET RNA, into GAM1699 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26379] It is appreciated that GAM1699 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1699 target genes. The mRNA of each one of this

plurality of GAM1699 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1699 RNA, herein designated GAM RNA, and which when bound by GAM1699 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1699 target proteins.

[26380] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1699 gene, herein designated GAM GENE, on one or more GAM1699 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26381] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1699 correlate with, and may be deduced from, the identity of the target genes which GAM1699 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26382] Nucleotide sequences of the GAM1699 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1699 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1699 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1699 are further described hereinbelow with reference to Table Table1.

[26383] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1699 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[26384] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 1700(GR1700) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at

least one target gene, the function and utility of which at least one target gene is known in the art.

[26385] GR1700 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR1700 gene was detected is described hereinabove with reference to Figs. 6–15.

[26386] GR1700 gene encodes GR1700 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[26387] GR1700 precursor RNA folds spatially, forming GR1700 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR1700 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR1700 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed–reversed sequence of the second half thereof, as is well known in the art.

[26388] GR1700 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellu–

lar enzymatic activity into at least 2 separate GAM precursor RNAs, GAM135 precursor RNA and GAM136 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[26389] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM135 RNA and GAM136 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[26390] GAM135 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM135 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM135 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM135 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[26391] GAM136 RNA, herein schematically represented by GAM2

binds complementarily to a target binding site located in an untranslated region of GAM136 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM136 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM136 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[26392] It is appreciated that specific functions, and accordingly utilities, of GR1700 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR1700 gene: GAM135 target protein and GAM136 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM135 and GAM136

[26393] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 1701 (GR1701) gene, which encodes an operon-like cluster of novel micro RNA-like

genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[26394] GR1701 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR1701 gene was detected is described hereinabove with reference to Figs. 6-15.

[26395] GR1701 gene encodes GR1701 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[26396] GR1701 precursor RNA folds spatially, forming GR1701 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR1701 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR1701 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[26397] GR1701 folded precursor RNA, herein designated GR

FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM250 precursor RNA and GAM251 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[26398] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM250 RNA and GAM251 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[26399] GAM250 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM250 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM250 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM250 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[26400] GAM251 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM251 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM251 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM251 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[26401] It is appreciated that specific functions, and accordingly utilities, of GR1701 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR1701 gene: GAM250 target protein and GAM251 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM250 and GAM251

[26402] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 1702(GR1702) gene, which en-

codes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[26403] GR1702 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR1702 gene was detected is described hereinabove with reference to Figs. 6-15.

[26404] GR1702 gene encodes GR1702 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[26405] GR1702 precursor RNA folds spatially, forming GR1702 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR1702 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR1702 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[26406] GR1702 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM749 precursor RNA and GAM750 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[26407] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM749 RNA and GAM750 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[26408] GAM749 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM749 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM749 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM749 target protein, herein schematically

represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[26409] GAM750 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM750 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM750 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM750 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[26410] It is appreciated that specific functions, and accordingly utilities, of GR1702 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR1702 gene: GAM749 target protein and GAM750 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM749 and GAM750

[26411] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to

here as Genomic Record 1703(GR1703) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[26412] GR1703 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR1703 gene was detected is described hereinabove with reference to Figs. 6-15.

[26413] GR1703 gene encodes GR1703 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[26414] GR1703 precursor RNA folds spatially, forming GR1703 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR1703 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR1703 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the sec-

ond half thereof, as is well known in the art.

[26415] GR1703 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM854 precursor RNA and GAM855 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[26416] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM854 RNA and GAM855 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[26417] GAM854 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM854 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM854 target RNA, herein schematically represented by GAM1 TARGET

RNA into GAM854 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[26418] GAM855 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM855 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM855 target RNA into GAM855 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[26419] It is appreciated that specific functions, and accordingly utilities, of GR1703 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR1703 gene: GAM854 target protein and GAM855 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM854 and GAM855

[26420] Fig. 16 further provides a conceptual description of novel

bioinformatically detected regulatory gene, referred to here as Genomic Record 1704(GR1704) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[26421] GR1704 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR1704 gene was detected is described hereinabove with reference to Figs. 6-15.

[26422] GR1704 gene encodes GR1704 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[26423] GR1704 precursor RNA folds spatially, forming GR1704 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR1704 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR1704 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is

at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[26424] GR1704 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1442 precursor RNA and GAM1443 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[26425] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1442 RNA and GAM1443 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[26426] GAM1442 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1442 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1442 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1442 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[26427] GAM1443 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1443 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1443 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1443 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[26428] It is appreciated that specific functions, and accordingly utilities, of GR1704 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR1704 gene: GAM1442 target protein and GAM1443 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function

of these target genes is elaborated hereinabove with reference to GAM1442 and GAM1443

[26429] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 1705 (GR1705) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[26430] GR1705 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR1705 gene was detected is described hereinabove with reference to Figs. 6-15.

[26431] GR1705 gene encodes GR1705 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[26432] GR1705 precursor RNA folds spatially, forming GR1705 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR1705 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the

fact that the nucleotide sequence of GR1705 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[26433] GR1705 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1566 precursor RNA and GAM1567 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[26434] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1566 RNA and GAM1567 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[26435] GAM1566 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in

an untranslated region of GAM1566 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1566 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1566 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[26436] GAM1567 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1567 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1567 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1567 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[26437] It is appreciated that specific functions, and accordingly utilities, of GR1705 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR1705 gene:

GAM1566 target protein and GAM1567 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1566 and GAM1567

[26438] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 1706 (GR1706) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[26439] GR1706 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR1706 gene was detected is described hereinabove with reference to Figs. 6-15.

[26440] GR1706 gene encodes GR1706 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[26441] GR1706 precursor RNA folds spatially, forming GR1706 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR1706 folded pre-

cursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR1706 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[26442] GR1706 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1673 precursor RNA and GAM1674 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[26443] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1673 RNA and GAM1674 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of

Fig. 8.

[26444] GAM1673 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1673 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1673 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1673 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[26445] GAM1674 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1674 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1674 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1674 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[26446] It is appreciated that specific functions, and accordingly utilities, of GR1706 gene, herein designated GR GENE,

correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR1706 gene: GAM1673 target protein and GAM1674 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1673 and GAM1674

[26447] BIBLIOGRAPHY

[26448] It is appreciated by persons skilled in the art that the present invention is not limited by what has been particularly shown and described hereinabove. Rather the scope of the present invention includes both combinations and subcombinations of the various features described hereinabove as well as variations and modifications which would occur to persons skilled in the art upon reading the specifications and which are not in the prior art.

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